	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	3 2 2 8 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
OM protein - pro	OM protein - protein search, using sw model	ММ
Run on:	<pre>September 7, 2004, 19:24:27 ; Search time 16 Seconds (without alignments) 12.906 Million cell updates/sec</pre>	2 W W W C
Title: Perfect score: Sequence:	US-09-931-009A-2 25 1 GPRP 4	0 60 44 4
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	ਗਾ ਹਾ ਹਾ
Searched:	389414 Begs, 51625971 residues	יייי
Total number of	Total number of hits satisfying chosen parameters: 11020	
Minimum DB seq length: 0 Maximum DB seq length: 4	ngth: 0 ength: 4	ւ Մ (Մ (Մ (Մ
Post-processing:	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 65 summaries	
Database :	<pre>Issued Patents AA:* 1: /cgn2 6/ptodata/2/iaa/5A_COMB.pep:* 2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep:* 3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:* 4: /cgn2 6/ptodata/2/iaa/B_COMB.pep:* 5: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /cgn2 6/ptodata/2/iaa/PcTUS_COMB.pep:*</pre>	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Appli	Appli	Appli	Appli	Appli	Appli	Appli		Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	, Appl			5425936	433940	Appli	Appli	, Appl	Appli	Appli
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-	Description	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Patent No	Patent No.	Patent No	Sequence	Seguence	Sequence	Sequence	Sequence
ស៊		53-5	9-00	181A-1	174-5	59-2	827A-1	4	7-	181-2	65	395~5	448-6	3-640-4	-847-6	-08231-6	1542-4	-034A-6	-034A-12	168B-1				-679A-9	759-1	-897A-12	-014-8	1270-9
SUMMARIES		07-934-5	US-07-932-200-6	08-022-3	US-08-225-4	US-08-365-7	US-08-475-8	38	47	US-08-753-78	US-08-993-1	US-08-611-3	9-54	9-24	3-92	PCT-US93-06	PCT-US95-07542	-917	-917	-98	5425936-4	5936	3940-1	16	8-365	-08-213-8	-476	CT-US92-11
	Ð.	US-07	us-	US-08	us-	us-	us-	us-	us-	us-	us-	US-	US-0	US-0	US-08	泛	Б	US-0	US-07	US-09	542	542	543	'n	0-50	-SD	US-08	PC
	DB	-	-	Н	Н	٦	Н	0	ď	7	m	m	4	4	4	ហ	ស	-	н	4	9	9	9	н	Н	ᠬ	7	Ŋ
	Query Match Length	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4,	4	4	4	4	4	٣	m	e	m	Э
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	76.0	76.0	76.0	76.0	76.0	76.0	72.0	72.0	ď	72.0	72.0
	Score	25	23	25	25	25	25	25	25	25	25	25	25	25	25	25	25	19	19	19	19	19	19	18	18	18	18	18
	Result No.	н	7	m	4	S	9	7	α	σ	10	11	12	13	14	15	16	17	18	19	20	21		23	24	25	26	27

Sequence 7, Appli	equence 8,	equence 9,	equence 1,	equence 2,	equence 50,	equence 9,	equence 4,	equence 50,	equence 50,	e 50,	equence 4,	equence 11,	equence 4,	equence 11,	equence 30,	equence 30,	equence 28,	equence 9,	equence 30,	eguence 28,	equence 28,	equence 7,	equence 8,	equence 9,	equence 75	equence 35	w	equence 30	equence 9,	equence 10	equence 14	quence 30	equence 30	equence 26	equence 9,		9
-07-932-200	-07-932-200-	-932-200-	-07-776-25	-07-776-257-	-08-127-351-	-08-095-162-	-08-365-759-	-08-480-367B-	-08-487-221A-5	-08-480-370-5	-08-294-434-4	-08-294-434-	-08-457-166-4	-08-457-166-1	-08-299-636-	-08-279-155-3	-08-464-456-2	-08-470-220A-	38-703-988A-	38-463-052-2	-08-480-551-2	-08-387-749-	-08-387-749-	-08-387-749-	-08-922-267A-	-08-685-589A-3	-08-685-589A-3	-08-612-842-3	-08-967-37	-08-927-128-1	-09-219-849-	054A-3	-08-958-993A-	-08-959-206A-2	9-505-99	-08-278-774-	-09-925-715-
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4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
8 18 72.	18 72.	0 18 72.	1 18 72.	2 18 72.	3 18 72.	4 18 72.	5 18 72.	6 18 72.	7 18 72.	38 18 72.0	9 18 72.	0 18 72.	1 18 72.	2 18 72.	3 18 72.	4 18 72.	5 18 72.	6 18 72.	7 18 72.	8 18 72.	9 18 72.	0 18 72.	1 18 72.	2 18 72.	3 18 72.	4 18 72.	5 18 72	6 18 72.	7 18 72.	8 18 72.	9 18 72.	0 18 72.	1 18 72.	2 18 72.	3 18 72.	4 18 72.	5 18 72.

ALIGNMENTS

RESULT 1
US-07-934-553-5
| Sequence 5. Application US/07934553
| Sequence 5. Application US/07934553
| Patent No. 5144690
| GENERAL INFORMATION:
| APPLICANT: PATTERSON, ROY
| APPLICANT: PATTERSON, ROY
| APPLICANT: PATTERSON, ROY
| APPLICANT: PATTERSON, ROY
| APPLICANT: TILEOF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
| TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
| NUMBER OF SEQUENCES: |
| CORRESPONDENCE ADDRESSE |
| ADDRESSE | TILTON, FALLON, LUNGMUS & CHESTNUT STREET: 100 SOUTH WACKER DRIVE CITY: CHICAGO STATE: ILLINOIS COUNTRY: USS OFFWATE READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ISM PC COMPATISH POSONO-DOSAMS: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: PRICA APPLICATION DATA: PRICA APPLICATION DATA: APPLICATION DATA: PRICA APPLICATION DATA: APPLICATION PURBER: US 07/705,071
| FILING DATE: 24-MAY-1991
| ATTORNEY/AGENT INFORMATION:

```
PAPELICANT: Stuber, Werner
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
ITILE OF INVENTION: Preparation Thereof and Agents Containing These as
ITILE OF INVENTION: Freparation Thereof and Agents Containing These as
ITILE OF INVENTION: Freparation Thereof and Agents Containing These
ITILE OF INVENTION: Freparation Thereof and Agents Containing These
NUMBER OF SEQUENCES: 22
CORRESSER: Finnega, Henderson, Farabow, Garrett & ADDRESSER: Finnega, Henderson, Farabow, Garrett & ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
CITY: Washington
CITY: Washington
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
CITY: Washington
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
CITY: Washington
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
CITY: Washington
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington DATA:
APPLICATION WITHER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION WITHER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION UNDER: 105-1054-10100
TELECOMMUNICATION NUMBER: 05-1054-10100
TELECOMMUNICATION NIFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Patterson, Roy
APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: 1gE Mediated Allergies
TITLE OF SOURNCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
                                                                                                                                                Sequence 1, Application US/08022381A Patent No. 5478810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO. SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / MOLECULE TYPE: peptide US-08-022-381A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GPRP 4
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                 1 GPRP
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US-08-225-474-5
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Patent No. 5366862

GENERAL INFORMATION:

APPLICANT: VENTOW, DUANE L.

APPLICANT: LE BRETOW, GUY

TITLE OF INVENTION: WEFUL PEPTIDES

NUMBER OF SEQUENCES: 20

NUMBER OF SEQUENCES: 20

SERRESPONDENCE ADDRESS:

ADDRESSE: BROWDY AND NEIMARK

STREET: 419 SEVENTH STREET, N.W.

CITY: MACHINGTON

STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Length 4; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 25; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,200
FILING DATE: 21-AUG-1992
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFRENCE/DOCKET NUMBER: VENTON-1B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S02-628-5197
TELEFAX: 202-737-3528
TELEX: 24833
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                     NU-9033CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NAME: FENTRESS, SUSAN B

REGISTRATION NUMBER: 31,327

REFERENCE/POCKET NUMBER: NU-91

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/456-8000

INFORMATION FOR SEQ ID NO: 5;

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

ITYPE: AMINO ACID

STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 amino acids
                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-07-934-553-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-932-200-6
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Gaps

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CLASSIFICATION: 436
PRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 24-FEB-1993
FILING DATE: 24-FEB-1993
APPLICATION DATA:
APPLICATION NUMBER: 06-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: 00h.son, Lori-Ann
REGISTRATION NUMBER: 34,496
REFERENCE/DOCKET NUMBER: 05552.1054-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO:
TELEFAX: (202) 408-4408
INFORMATION FOR SEQ ID NO: (1:)
SEQUENCE: ARRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08475827A Patent No. 5607858
REGISTRATION NUMBER: 35,391
REFRENCE/DOCKET NUMBER: 0555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-400
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-365-759-2
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08365759
Parent No. 5563041
GENERAL INFORMATION:
APPLICANT: Reers, Martin
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES:
CORRESPONDENCE 4
CORRESPONDENCE Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 20005-3315
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEACENTIN Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,759
PTLING DATE: 20-DEC-1994
                                                                                                                                                                                                  COFTANTA STATEM:
COFTANTA STATEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/25,474
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AQG 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-AMY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REFERENCE/DOCKET NUMBER: US 926
REFERENCE/DOCKET NUMBER: UN 9033-CIP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1300 I Street, N.W., Suite 600 CITY: Washington STATE: D.C.
    100 S. Wacker Drive, Suite 960
                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (312) -456-800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-225-474-5
                                                                                       ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                        Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Stuber, Werner

APPLICANT: Elickenscher Karl

TITLE OF INVENTION: Peptide Amides, Processes For the

TITLE OF INVENTION: Peptide Amides, Processes For the

TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors

TUTLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSE: 22

CORRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA Gaps ö 100.0%; Score 25; DB 1; Length 4; 100.0%; Pred. No. 3e+05; CONTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Jac PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
COMPATE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: 07-UNN-1995 STRANDEDNESS: TOPOLOGY: lin ö

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Gaps
Gaps
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Sequence 81, Application US/08747137
Sequence 81, Application US/08747137
Sequence 81, Application US/08747137
GENERAL INFORMATION:
APPLICANT: YEN, Richard C.K.
ATILE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR TITLE OF INVENTION: THERAPBUTIC AND DIAGNOSTIC USE NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two man of Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUNITY: USA

CUNTRIE: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
CONTRARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/212,546
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,831
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: US 07/9192
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: US 07/9192
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/9192
FILING DATE: US 07/9192
FILING DATE: US 07/9191
ATTORNEY/AGENT INFORMATION:
AND ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMETION INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT IN
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US-08-753-781-2
/ Sequence 2, Application US/08753781C
/ Patent No. 5951981
/ PATENT NO. 5951981
/ PATENT NFORMATION:
/ APPLICANT: Markland Jr., Francis S.
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4; Conservative
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STRANDEDNESS: not
                                                               1 GPRP 4
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                                                                                                                                                                                                                                                  US-08-747-137-81
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Matches
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                                                 100.0%; Score 25; .DB 1; Length 4; tilarity 100.0%; Pred. No. 3e+05; Conservative 0; Mismatch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: VENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: HE BRETON, GUY
TITLE OF INVENTION: WETHOD FOR GENERATING AND SCREENING
TITLE OF INVENTION: USEPUL PEPTIDES
NUMBER OF SECUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,749
FILING DATE: 21-Peb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21-Feb-1995
CLASSIFICATION: 435
PRIOR PAPELICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08231
FILING DATE: 09-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/932,200
FILING DATE: 21-AUG-1992
RECOR PAPELICATION NUMBER: US 07/813,315
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATE: APPLICATION NUMBER: PCT/US91/00891
FILING DATE: 14-FEB-1991
PRIOR APPLICATION NUMBER: PCT/US91/00891
FILING DATE: 14-FEB-1991
PRIOR APPLICATION NUMBER: PCT/US91/00891
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/480,865
FILING DATE: 14-FEB-1991
ATTORNEY/AGENT INFORMATION:
AND TO COMPANY NUMBER: US 07/480,865
FILING DATE: 114-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTON=1C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08387749
Patent No. 5814460
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 amino acida
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MOLECULE TYPE: peptide
; MOLECULE TYPE: peptide US-08-475-827A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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STRANDEDNESS: sin
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20004
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Best Local Similarity
                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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Sequence 4, Application US/09243640 Patent No. 6521211
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-540-448-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-243-640-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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| Sequence 6, Application US/08993165A
| Sequence 6, Application US/08993165A
| Patent No. 612393
| GENERAL INFORMATION:
| APPLICANT: Unger, Evan C
| APPLICANT: Wunglu
| TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
| TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
| FILE REFERENCE: UNGRIZ24
| CURRENT APPLICATION NUMBER: US/08/993,165A
| NUMBER OF SEQ ID NOS: 49
| SOFTWARE: Ratentin Ver. 2.1
| LENGTH: 4
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               APPLICANT: Swenson, Stephen
APPLICANT: Flores Sanchez, Eladio
ITLLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
FILE REFERENCE: DITI 124
CURRENT APPLICATION NUMBER: US/08/753,781C
CURRENT PILING DATE: 1996-12-02
NUMBER OF GEQ ID NOS: 40
SOFTWARF: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH:
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100.0%; Score 25; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels
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TAN, PARIS S. T.
TAN, PARIS S. T.
TANATRUI, SHIN'ICHI
IWASAKI, TALSUKE
TITLE OF INVENTION: NOVEL ENDOPEPTIDASE
NUMBER OF ENDURES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-611-395-5
; Sequence 5, Application US/08611395
; Patent No. 6168939
                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
APPLICANT: Bush, Larry R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GPRP 4
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                                                                                                                                                                                                                                                                                                                                 US-08-753-781-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
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Sequence 6, Application US/09540448

Patent No. 6403056

GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TILLE OF INVENTION: Charged Lipids and Uses For The Same FILE REPERSENCE: UNGRISS2
CURRENT APPLICATION NUMBER: 08/995,353

PRIOR APPLICATION NUMBER: 08/925,353

PRIOR FILING DATE: 1997-09-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 25; DB 3; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,395
                                                                                                                                                                                                 FILING DATE: 06-Mar-1996
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA PREJESTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPINGS: «UNKNOWID»; TOPOLOGY: LINear; ; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-08-611-395-5
                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 248-
INFORMATION FOR SEQ ID NO: (5:
SEQUENCE CHARACTERISTICS
ZIP: 02110
COMPUTER READABLE FORM:
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APPLICANT: LE BRETON, GUY
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
TITLE OF INVENTION: USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SERVENTH STREET, N.W.
CITY: WASHINGTON
STREET: 0.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: PATENTIAL POSSION:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: PATENTIAL POSSION:
MEDIUM TYPE: Ploppy disk
COMPUTER: PATENTIAL POSSION:
MEDIUM TYPE: Ploppy disk
COMPUTER: PATENTIAL POSSION:
MEDIUM TYPE: Ploppy disk
COMPUTER: PATENTIAL POSSION:
APPLICATION DATA:
ATTAC
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100.0%; Score 25; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC
TITLE OF INVENTION: DOMAINS OF TRANSMEMBRANE RECEPTORS
NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: FIGHT Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
GURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07542
FILING DATE: 13-UWN 1995
BRICH APPLICATION DATA:
APPLICATION NUMBER: USSN 08/260,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P. 28,005
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTONIC.PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
PCT-US95-07542-4
; Sequence 4, Application PC/TUS9507542
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-JUN 1994
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 4 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLGGY: linear
MOLECULE TYPE: peptide
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MOLECULE TYPE: pepti
HYPOTHETICAL: NO
FRAGMENT TYPE: inter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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TELEX: 2'
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  GENERAL INFORMATION:
APPLICANT: Unger, Evan C
APPLICANT: Wu, Guanli
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NO. 6521211e1 Methods Of Imaging And Treatment With Targeted
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/243,640
CURRENT APPLICATION NUMBER: US/08/60,032
PRIOR FILING DATE: 1996-06-06
PRIOR FILING DATE: 1996-06-06
PRIOR FILING DATE: 1996-06-06
PRIOR FILING DATE: 1996-06-07
PRIOR APPLICATION NUMBER: 08/497,684
PRIOR FILING DATE: 1996-06-07
PRIOR APPLICATION NUMBER: 08/497,684
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08929847
Patent No. 6548047
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TILLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
FILE REPRENCE: BMS041
CURRENT APPLICATION NUMBER: US/08/929,847
CURRENT PILING DATE: 1997-09-15
SOUTHWARE: PatentIn version 3.1
SEQ ID NO.96
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence
JS-09-243-640-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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100.0%; Score 25; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application PC/TUS9308231
GENERAL INFORMATION.
APPLICANT: VENTON. DUANE L.
APPLICANT: HOPFINGER, ANTON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Seguence
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Best Local Similarity
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PCT-US93-08231-6
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Sequence 6, Application US/07917034A

Patent No. 1842792.

GENERAL INFORMATION:
APPLICANT: Meyer, Thomas, Pohlner, Johannes, Schumacher,
APPLICANT: Meyer, Thomas, Pohlner, Of Recombinant Proteins Using 1gA Proteases
CORRESPONDENCE ADDRESS:
ADDRESSEE: Falfe & Lynch
STREET: 805 Third Avenue
CITY: New York
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                                                                                                    100.0%; Score 25; DB 5; Length 4; llarity 100.0%; Pred. No. 3e+05; Conservative 0; Mismatches 0; Indels
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                         Ligand sequence recognized by integrin
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100.0%; Pred. No. 3e+05;
iive 0; Mismatches
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CURRENT APPLICATION DATA:
FILING DATE: 19920830
CLASSIFICATION NUMBER: US/07/917,034A
FILING DATE: 19920830
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00192
FILING DATE: 1-Feb-1991
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 17-May-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 922.1
FILING DATE: 17-May-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 921.3
FILING DATE: 17-May-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 03 149.7
FILING DATE: 3-Feb-1990
ATTONNEY, AGENT INFORMATION:
ANNEY: HARCALION NUMBER: DE 40 03 149.7
FILING DATE: 3-Feb-1990
ATTONNEY, CARRET INFORMATION:
ANNEY: HARCALION NUMBER: DE 40 03 149.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hanson, No. 5427927man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: HUBR 1018
INFORMATION FOR SEQ ID NO: 6:SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I: Diskette, 5.25 incl
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 3; Conserv
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ORIGINAL SOURCE:
ORGANISM: Liq
                                                                                                                                                                                                        1 GPRP 4
                                               PCT-US95-07542-4
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APPLICANT: Witter, David
TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED PEPTIDOMIMETICS AS BETA-TURN
TITLE OF INVENTION: TEMPLATES AND MODULATORS OF SH3 DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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US-07-917-034A-12
| Sequence 12, Application US/07917034A |
| Sequence 12, Application US/07917034A |
| Sequence 12, Application US/07917034A |
| Patent No. 5437927 |
| GENERAL INFORMATION: Patent No. 5477927 |
| APPLICANT: Meyer, Thomas, Pohlner, Johannes, Schumacher, APPLICANT: Meyer, Thomas, Pohlner, Johnson Office Offi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/917,034A FILING DATE: 19920830 CLASSIPICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/EP91/00192 PRIOR APPLICATION NUMBER: DE 40 39 415.8 FILING DATE: 10-Dec-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE 40 39 415.8 FILING DATE: 10-Dec-1990 PRIOR APPLICATION NUMBER: DE 40 15 922.1
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FILING DATE: 17-May-1990
REIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 15 921.3
FILING DATE: 17-May-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 03 149.7
FILING DATE: 3-Feb-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hanson, No. 5427927man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09086168B Patent No. 6638941 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect CURRENT APPLICATION DATA
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; TOPDLOGY: linear
; MOLEGULE TYPE: protein
US-07-917-034A-12
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Matches 3; Conserv
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US-09-086-168B-1
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APPLICATION NUMBER: US/08/834,259
FILING DATE: 17-AUG-1990
PRIOR APPLICATION NUMBER: 548,388
FILING DATE: 06-JUL-1989
APPLICATION NUMBER: 395,482
FILING DATE: 18-AUG-1989
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                                                                                                                      Length 4;
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STREET: 100 Peachtree Street, Suite 3200
CITY: Atlanta
STATE: 260rgia
COUNTRY: U.S.
ZIP: 30303
COMPUTER: BIOPY disk
COMPUTER: BIN PC compatible
COMPUTER: ParcentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/816,679A
FILING DATE: 19920103
CLASSIFICATION NUMBER: US 07/730040
FILING DATE: 12-UUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/730040
FILING DATE: 12-UUL-1991
PRIOR APPLICATION NUMBER: US 07/730040
FILING DATE: 30-DEC-1988
                                                                                                                      DB 6;
3e+05;
                                                                                                                                                                                      Mismatches
                                                                                                                         Score 19;
Pred. No.
                                                                                                                      Query Match
Best Local Similarity 100.0%; Pr
Matches 3; Conservative 0;
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5425936-8
SEQ ID NO:8:
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5433940-1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 13-JUL-1992
FILING DATE: 31-JUL-1992
PRICA APPLICATION DATA:
APPLICATION NUMBER: 652,929
FILING DATE: 08-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
5421935 - .
FALENT NO. 5425936
; APPLICANT: MARAGANORE, JOHN M.; JABLONSKI, JO-ANN M.; BOURDON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%; Score 19; DB 4; Length 4; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 76.0%; Score 19; DB 6; Length 4; Similarity 100.0%; Pred. No. 3e+05; 3; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/924,549
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 652,929
FILING DATE: 08-F8B-1991
APPLICATION NUMBER: 549,388
FILING DATE: 06-JUL-1990
APPLICATION NUMBER: 395,482
FILING DATE: 18-AUG-1989
                    CURERY APPLICATION NUMBER: US/09/086,168B CURRENT FILING DATE: 1998-05-28 NUMBER OF SEQ ID NOS: 5 SOFTWARE: Patentin version 3.1 SEQ ID NO 1 LENGTH: 4
                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: SH3 test peptide FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1). (4)
COTHER INFORMATION: Synthetic Peptide US-09-086-1688-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 549,388
FILING DATE:06-JUL-1990
APPLICATION NUMBER: 395,482
FILING DATE: 18-AUG-1989
                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 3; Conservative
   FILE REFERENCE: 60384-B
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Best Local Similarity
Matches 3; Conserv
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5425936-4
;Patent No.
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APPLICANT: Iwata, Kenneth K
APPLICANT: Foulkes, J. Gordon
APPLICANT: Foulkes, J. Gordon
APPLICANT: Haley, John D
TITLE OF INVENTION: TISSUE-DERIVED TUMOR GROWTH
TITLE OF INVENTION: METHODS OF PREPARATION AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STRIET: New York
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Protease Mediated Drug Delivery System NUMBER OF SEQUENCES: 18
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentl Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentl Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentl Release #1.0, Version #1.30 (EPO)
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/213,897A
PRICATION NUMBER: US 07/593,867
PRICATION NUMBER: US 07/593,867
PRICATION NUMBER: US 07/833,183
PRICATION NUMBER: US 07/833,183
FILING DATE:
APPLICATION NUMBER: US 07/833,183
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                                                              72.0%; Score 18; DB 1; Length 3; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 1;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 3e-Matches 3; Conservative 0; Mismatches
                                                                                                                                                                                                                                                   US-08-213-897A-12

Sequence 12, Application US/08213897A

Patent No. 5618790

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08476014
Patent No. 5871724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                              Query Match 72.0
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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US-08-365-759-1
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US-08-476-014-8
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                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1..3
; OTHER INFORMATION: /note= "Thrombin Cleavage Site"
US-07-816-679A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALGAME: Pabet, Detrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF130
TELEPAN: 404-572-6508
TELEPAN: 404-572-6508
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683682
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GPR 3
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US-08-365-759-1
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Sequence 7, Application US/07932200

Patent No. 5366862

GENERAL INFORMATION:
APPLICANT: WENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
TITLE OF INVENTION: WEFFOR GENERATING AND SCREENING
TITLE OF INVENTION: USFFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: NEIMARK
STREET: A19 SEVENTH STREET, N.W.
CITY: WARMINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIPE: 20004
COUNTRY: U.S.A.
ZIPE: 20004
COUNTRY: U.S.A.
ZIPE: 20004
COUNTRY: U.S.A.
STATE: U.S.A.
ZIPE: 20004
COUNTRY: U.S.A.
STATE: U.S.A.
STATE: U.S.A.
ZIPE: 20004
FILLING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRATING SYSTEM: US/07/932,200
FILLING DATE: 21-AUG-1992
CURRAINS APPLICATION BATE:
APPLICATION: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COTHER INFORMATION: /note= "Thrombin Cleavage Site"; CT-US92-11270-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.0%; Score 18; DB 5; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches (
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PP: VENTON=1B
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NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENY
TELECOMMUNICATION: 1NFORMATION:
TELECHHONE: 202-628-5197
REFERENCE/DOCKET NUMBER: OW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-655
                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
FEATURE:
NAME/KEY: Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                         TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                        TYPE: AMINO ACID
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application PC/TUS9211270
GENERAL INFORMATION:
APPLICANT: Rezaie, Alireza
APPLICANT: Esmon, Charles T.
APPLICANT: Morrissey, James H.
TITLE OF INVENTION: Expression and Purification of
TITLE OF INVENTION: Recombinant Soluble Tissue Factor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUW TYEE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11270
FILING DATE: 19921229
FILOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816679
FILING DATE: 03-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/730040
FILING DATE: 12-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/730040
FILING DATE: 30-DEC-1988
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/683682
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: PABLE ABACE, PARTER AI, 284
   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOSTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,014
FILING DATE: 07-010-1995
FILING DATE: 07-010-1995
ATTORNEY/AGENT INFORMATION:
NAME: White: John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 8:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 8:
AND TO THE SEQUENCE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GPR 3
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Patent No. 54949612
GENERAL INFORMATION:
APPLICANT: Lepargneur, Jean-Pierre
APPLICANT: Contant epouse Pussard,
APPLICANT: Generate Generate Generate APPLICANT: Generate Generate APPLICANT: Martinoli, Jean-Luc
APPLICANT: Wartinoli, Jean-Luc
APPLICANT: Quentin, Geraci
TITLE OF INVENTION: Process for identifying Candida by
TITLE OF INVENTION: Process for identifying Candida by
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                            STATE: D.C.

COUNTRY! U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: FI-loppy disk

COMPUTER: IBM PC compatible

OFFRAMING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PARENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/932,200

FILING DATE: 21-AUG-1992

CLASSIFICATION: 435

ATTONENY/AGENT INFORMATION:

NAME: COOPER INFORM POSE PS 9.005

REGISTRATION NUMBER: 28,005

REGISTRATION INFORMATION:

TELEBRAX: 202-737-3528

TELERAX: 202-737-3528

TELESCOMMUNICATION INFORMATION:

TELESCOMMUNICATION SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/776,257
FILING DATE: 19911119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.0%; Score 18; DB 1;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Jacobson, Price Holman & Stern STREFT: 400 Seventh Street N.W. CITY: Washington D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/PR/91/00233
FILING DATE: 23-MRR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-932-200-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                           WASHINGTON
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                                                                                                                                                                                                                                                 Sequence 8, Application US/07932200
| Patent No. 536862 |
| GENERAL INFORMATION: |
| APPLICANT: VENDOW, DUANE L. |
| APPLICANT: HOPFINGER, ANTON J. |
| APPLICANT: HOPFINGER, ANTON J. |
| APPLICANT: BEREYOW, GUY |
| TITLE OF INVENTION: WETHOD FOR GENERATING AND SCREENING |
| TITLE OF INVENTION: USEFUL PEPTIDES |
| NUMBER OF SEQUENCES: |
| ADDRESSEE: BROWDY AND NEIMARK |
| STREET: 419 SEVENTH STREET, N.W. |
| CILY: WASHINGTON |
| STATE: D.C. |
| COUNTRY: U.S.A. |
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/07932200
Patent No. 5366862
GENERAL INFORMATION:
APPLICANT: VEWTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: LE BRETON, GUY
TITLE OF INVENTION: METHOD FOR GENERATING AND SCREENING
TITLE OF INVENTION: USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%; Score 18; DB 1; Length 4; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: ILM SATEM: PC-DOS/NS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,200
FLING DATE: 21-AUG-1992
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: VENTON=1B
TELEDCOMMUNICATION INFORMATION:
TELEDCOMMUNICATION INFORMATION:
TELEDFAN: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS: LENGTH: 4 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide US-07-932-200-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                    1 GPR 3
                                                                              1 GPR 3
                                                                                                                                                                                                        RESULT 29
US-07-932-200-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-932-200-9
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Gaps

Sequence 2, Application US/07776257;
Sequence 2, Application US/07776257;
Patent No. 5449612
GENERAL INFORMATION:
APPLICANT: Lepargneur, Jean-Pierre
APPLICANT: Genevieve Pussard,
APPLICANT: Martinoli, Jean-Luc
APPLICANT: Wartinoli, Jean-Luc
APPLICANT: Quentin, Gerard
TITLE OF INVENTION: means of Chromogenic Substances
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price Holman & Stern
ADDRESSEE: Jacobson, Price Holman & Stern Query Match 72.0%; Score 18; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/776,257
FILING DATE: 19911119
CLASSIFICATION NUMBER: US/07/776,257
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00233
APPLICATION NUMBER: PCT/FR/91/00233
FILING DATE: 23-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: ADIANA, John C
REGISTRATION NUMBER: 5885/P-5449NA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: TELEFAX: (202) 393-5350
TELEFAX: (202) 393-5350
TELEX: RCA 246593 IDEA UR
INFORMATION FOR SEQ ID NO. 2: SEQUENCE CHARACTERISTICS: TOPOLOGY: linear US-07-776-257-2

Gaps ..

Query Match
Best Local Similarity 100.
Matches 3; Conservative

APPLICANT: Stout, Jay
APPLICANT: Henriksen, Dennis
APPLICANT: Henriksen, Dennis
APPLICANT: Marning, Shane
APPLICANT: Manning, Shane
TITLE OF INVENTION: Enzymatic Method for Modification of
TITLE OF INVENTION:
WHABER OF SEQUENCES: 26

Sequence 9, Application US/08095162 Patent No. 5512459 GENERAL INFORMATION: APPLICANT: Wagner, Fred W.

RESULT 34 US-08-095-162-9

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APPLICANT: BELIKKA Jr, BENJAMIN A.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: WOOD, RIGHARD
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
TITLE OF INVENTION: CONSTRUCTS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.0%; Score 18; DB 1; Length 4; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington CITY: Arginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSIEM: PC-DOS/MS-DOS
OPERATING SYSIEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,351
FILING DATE: 28-SEP-1993
CLASSIFICATION: 534
ATTORNEY/AGENT INFORMATION:
NAME: VILLAGOTECA, Gilberto M.
NAME: VILLAGOTECA, Gilberto M.
REGIGERATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-004-44.
TELECOMMUNICATION INFORMATION:
TELEPRAX: (703) 413-220
TELEPRAX: (703) 413-220
TELEPRAX: (703) 413-220
TELEPRAX: A8885 OPAT UR
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino_acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                 Sequence 50, Application US/08127351
Patent No. 5449761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-127-351-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                           GENERAL INFORMATION:
1 GPR 3
                                                                                                                                          US-08-127-351-50
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Gaps

us-09-931-009a-2.closed.rai

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Gaps
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US-08-4980-3678-50
IS-08-4980-3678-50
Sequence 50, Application US/08480367B
Patent No. 557828
GENERAL INFORMATION:
APPLICANT: BELLINKA JF, BENJAMIN A.
APPLICANT: ALVAREZ, VERNON L.
APPLICANT: MODO, RICHARD
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
TITLE OF INVENTION: CONSTRUCTS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          Query Match 72.0%; Score 18; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%; Score 18; DB 1; Length 4; 100.0%; Pred. No. 3e+05; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/ADATE: 07-06-95
CLASSIFICATION: 424
ATTORNEY/ADATI INFORMATION:
NAME: 0/11acorta, dilberto M.
REGISTRATION NUMBER: 34,038
REFERENDE/DOCKET NUMBER: 2654-002A
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
                                                                                                                                                                                                   NAME/KEY: Modified-site
LOCATION: 4
COCHION: 4
US-08-365-759-4
US-08-365-759-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LOWE, PRICE, Leblanc & BECKER STREET: 99 Canal Center Plaza, Suite 300 CITY: Alexandria STATE: Virginia COUNTRY: U.S.A. ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luve.
                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-08-480-3678-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nacous 35
US-08-365-759-4

Sequence 4, Application US/08365759

TITLE OF INVENTION: Method for Determining Platelet

TITLE OF INVENTION: Aggregation

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.

ZIP: 2005-3315

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,759
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin M.
REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 05552.1378-00000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 36,49400
TELEFRAX: 202-408-4400
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,162
PILING DATE: 20-JUL-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,659
REFERENCE/DOCKET NUMBER: 28,659
REFERENCE/DOCKET NUMBER: 28,659
RELEPHONE: 612-332-5300
TELEPHONE: 612-332-9081
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1300 I Street, N.W., Suite 600 CITY: Washington STATE: D.C.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5512459west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.0
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-095-162-9
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GENERAL INFORMATION:

APPLICANT: Stout, Jay

APPLICANT: Coolidge, Thomas R.

APPLICANT: Wagner, Fred W.

APPLICANT: Coolidge, Thomas R.

APPLICANT: Wagner, Fred W.

APPLICANT: Wagner, Barton

TITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID

TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF

NUMBER OF SEQUENCES: 15

NUMBER OF SEQUENCES: 15

STREET: 3100 No. 5635371west Center

CITY: Minneapolis

CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
72.0%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
                             ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
STREET: 1755 S. Jefferson Davis Highway, Suite 400
STRIE: 12520
COMPUTER: U.S.A.
TIP: 22222
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Federase #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,370
FILING DATE:
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/127,351
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Villacotta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-004-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3200
TELEFAX: (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,434
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide US-08-480-370-50
NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GPR 3
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STATE: MI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
US-08-294-434-4
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                                                                                            Sequence 50, Application US/08487221A
Sequence 50, Application US/08487221A
Sequence 50, Application US/08487221A
PARTECANT: COUGHLIN, DANIEL J.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: MIVAREZ, VERNON L.
APPLICANT: MANATION: METAL-BINDING TARGETED POLYPEPTIDE
TITLE OF INVENTION: ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: USEGINIA
COUNTRY: U.S.A.
ZIP: 22202
STREET: USEGINIA
COUNTRY: U.S.A.
ZIP: 22202
SOFTWARE: VISION PARS:
COMPUTER: BAP PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALINGIN NAMER: US/08/487,221A
FILING BATE: OUT-UNN-1995
CLASSIFICATION NUMBER: US/08/487,221A
FILING DATE: US-SEP-1993
ATTORNEY APPLICATION NUMBER: US/08/487,321A
FILING DATE: US-SEP-1993
ATTORNEY APPLICATION NUMBER: 34,038
REFERENCE POCKET NUMBER: 34,038
REFERENCE POCKET NUMBER: 34,038
REFERENCE POCKET NUMBER: 4980-004-44
TELECOMMUTICATION INTERPRACTION:
TELECOMMUTICATION INTERPRECTOR
TELEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-400-370-50
Sequence 50, Application US/08480370
Fatent No. 5609MATION:
APPLICANT: BELINKA Jr, BENJAMIN A.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: WOOD, RICHARD;
APPLICANT: WOOD, RICHARD;
TITLE OF INVENTION: CONSTRUCTS
ITLE OF INVENTION: CONSTRUCTS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.0%; Score 18; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TOPOLOGY: """
ODECTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-487-221A-50
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Sequence 4, Application US/08457166
Patent No. 5556456
GENERAL INFORMATION:
APPLICANT: Stout, Jay
APPLICANT: Wagner, Fred W.
APPLICANT: Coolidge, Thomas R.
APPLICANT: Holmquist, Barton
TITLE OF INVENTION: ALPHA-CARRON FRACTIVE GROUP OF A RECOMBINAL AMINO ACID
TITLE OF INVENTION: ALPHA-CARRON REACTIVE GROUP OF A RECOMBINAL TITLE OF INVENTION: POLYBEPTIDE OR A PORTION THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.0%; Score 18; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        Query Match 72.0%; Score 18; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5656456west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER: READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,166
TLING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/091,751
FILING DATE: 13-7UL-1992
APTORNEY/AGENT INFORMATION:
NAME: NABION, Albin J.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 28,650
REFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4 amino acids
                                           TOPOLOGY: linear / MOLECULE TYPE: peptide US-08-294-434-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-457-166-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 40
US-08-294-434-11

i Sequence 11. Application US/08294434

patent No. 5635371

GENERAL INFORMATION:

APPLICANT: Stout, Jay

APPLICANT: Magner, Fred W.

APPLICANT: Colidge, Thomas R.

APPLICANT: Magner, Fred W.

APPLICANT: Modifie, Barton

ITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID

ITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT

ITLE OF INVENTION: POLYPEPTIDE.OR A PORTION THEREOF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSES: Merchant & Gould

STREET: 3100 No. 5635371west Center

CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 1; Lengtn 4; Pred. No. 3e+05; 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/294,434
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,798
FILING DATE: 13-JUL-1992
ATTOKNEY/ASENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
REPRENCE/COKET NUMBER: 8648.29-US01
TELECOMMUNICATION INFORMATION:
TELEFRANCE 612-332-5300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,798
FILING DATE: 13-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
NEGISTRATION NUMBER: 86.60
REFERENCE/DOCKET NUMBER: 86.829-US01
TELEPHONE: 612-332-9081
TELEPHONE: 612-332-9081
TELEPHONE: 612-332-9081
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%; Scc_
100.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-294-434-4
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Best Local Similarity
Matches 3; Conserv
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Gaps

us-09-931-009a-2.closed.rai

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPR 3
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US-08-299-636-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-279-155-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
Sequence 11, Application US/08457166

Patent No. 556456

GENERAL INFORMATION:

APPLICANT: Stout, Jay

APPLICANT: Coolidge, Thomas R.

APPLICANT: Holmquist, Barton

TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE

TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT

TITLE OF INVENTION: POLYBETIDE OR A PORTION THEREOF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

STREET: 3100 No. 5656456west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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US-08-299-636-30
US-08-299-636-30
Sequence 3.0, Application US/08299636
Partent No. 5659041
GENERAL INFORMATION:
APPLICANT: POLLAK, Alfred
APPLICANT: POLLAK, Robert A.
APPLICANT: DUNN-DUFAULT, Robert
ITILE OF INVENTION: HYDRAZINO-TYPE RADIONUCLIDE CHELATORS
ITILE OF INVENTION: HAVING AN N3S CONFIGURATION
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.0%; Score 18; DB 1; Length 4; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Nelson, Albin J.
REGISTRATION UNBER: 28,650
REFERENCE/DOCKET NUMBER: 8648.35-US-01
TELECOMOUNICATION INFORMATION:
TELEPHONE: 612-332-5300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US 07/912,798
FILING DATE: 13-ULI-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-457-166-11
                                                                                                                                                                                                                                                                                                                Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                         USA
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2 GPR 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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ADDRESSEE Folge & Larther

STREET: 3000 K Street, N.W., Suite 500

CITY: Ansingston

CONTY: Ansingston

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Sequence 9, Application US/08470220A
Patent No. 5707826
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-703-988A-30
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| Sequence 28, Application US/0846456
| TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Taging | TITLE OF INVENTION: Taging | NUMBER OF SEQUENCES: 37 | CORRESPONDENCE ADDRESS: ApplesSPEET: 10 South Wacker Drive Suite 3000 | STREET: 10 South Wacker Drive Suite 3000 | STREET: Illinois | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4;
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ZIP: 60606

COMPUTER FADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,456
FILING DATE: OS-UN 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5681541nax, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 36,303
REFERENCE/DOCKET NUMBER: 90,1104-V
TELEPHONE: 312 715 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 1;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 3e-Matches 3; Conservative 0; Mismatches
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-4810
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.0
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                      LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein US-08-279-155-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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RESULT 46 US-08-470-220A-9

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APPLICATION SEGRET, Fred W.

APPLICATION SEGRET, Fred W.

APPLICATION SEGRET, Prod W.

APPLICATION SECRETARIES Death of Particles APPLICATION SECRETARIES SEGRET SECRETARIES SEGRET SEGR
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Gaps
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; Sequence 28, Application US/08480551
; Fatent No. 5911394
; GENERAL INFORMATION:
    APPLICANT: Dean, Richard T
    TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Imaging
    NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: ADDRESSE:
    ADDRESSEE: ADDRESSE:
    ADDRESSEE: ADDRESSE:
    CITY: Chicago
    STREET: Illinois
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.0%; Score 18; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIPICATION: 530

RICA APPLICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/264,176
FILING DATE:
APPLICATION NUMBER: US 07/653,012
FILING DATE: 08-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCDONNELL, JOHN J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 90,1104
TELECHONE: 312 715 1000
TELECHONE: 312 715 1234
TELECHONE: 312 715 1000
TELEFAX: 312 715 1000
                                                                                                                                                                 Query Match
Best Local Similarity 100...
3; Conservative
        SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 amino acids
                                                                                                              , MOLECULE TYPE: peptide US-08-463-052-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide US-08-480-551-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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US-08-387-749-7
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Sequence 28, Application US/08463052;
Fatent No. 5788960;
GENERATION:
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Imaging NUMBER OF SEQUENCES: 37 CORRESPONDENCE ADDRESS: ADDRESSE: STREET: Il 0 South Wacker Drive Suite 3000 STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.0%; Score 18; DB 1; Length 4; llarity 100.0%; Pred. No. 3e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,052

FLING DATE: 05-JUN-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: No. 5788960nn, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 90,1104-V

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHORE: 312 715 1234
ZIP: 20005-5701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPAGE: BY SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING APPLICATION NUMBER: US/08/703,988A
FILING APPLICATION: 424
PRIOR APPLICATION WHERE: US/08/279,155
FILING BAPLICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WURRAY, ROBET B.
REGISTRATION NUMBER: 22-980
REFERENCE/DOCKET NUMBER: P8074-6011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLICGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 3; Conserv
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us-09-931-009a-2.closed.rai

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Sequence 7, Application US/08387749
Patent No. 5814460
GENERAL INFORMATION
APPLICANT: WINTON, DUANE L.
APPLICANT: WINTON, DUANE L.
APPLICANT: BESTON, GUY
TITLE OF INVENTION: USEFUL PEPTIDES
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NIMMARK
GITY: WASHINGTON
STREET: HOPPY AND NIMMARK
GITY: WASHINGTON
STREET: PLORGY AND NIMMARK
GITY: WASHINGTON
STREET: PLORGY GIS
COMPUTER READABLE FORM:
MEDIDY TYPE: PLORGY GIS
COMPUTER READABLE FORM:
MEDIDY TYPE: PLORGY GIS
COMPUTER: LIBM PC COMPACTION
OFFRATION STREET: LIBM PC COMPACTION
OFFRATION OFFRATION DATA:
APPLICATION NUMBER: US/08/3817,749
FILING DATE: 21-F6D-1995
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/932,200
FRICKS APPLICATION DATA:
APPLICATION NUMBER: US 07/932,200
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/932,200
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/933,315
FILING DATE: 11-F6D-1992
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/933,315
FILING DATE: 11-F6D-1992
FRICK APPLICATION NUMBER: US 07/933,315
FILING DATE: 14-FEB-1991
FRICK APPLICATION NUMBER: US 07/930,0831
FRICK APPLICATION UNMBER: US 07/930,0831
FRICK APPLICATION UNMBER: US 07/930,0831
FRICK APPLICATION UNM
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72.0%; Score 18; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels
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; MOLECULE TYPE: peptide
US-08-387-749-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
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Search completed: September 7, 2004, 19:32:52 Job time : 17 secs

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Aaw94617 Src homol Aao29624 Anti-angi Adc22266 Protein b Adc15592 Rho 110 l	Adc15585 Rho 110 1 Adc15559 Rho 110 1	Add52662 Anglogene Aay80482 Cell adhe Aab1977 Fibronect Abu60858 Peptide p	Aar26394 Sequence Aar32383 Fibrinoge Aar32384 Fibrinoge Aar32385 Fibrinoge	Aar48072 Biologica Aar48079 Intra/Int Aar49797 Semience	Aar49798 Sequence Aar49799 Sequence	Aar60327 Blood coa Aaw09862 Thrombin	Aar80052 Peptidase Aar80053 Peptidase Aar69071 Interconn	Aaw11088 Thrombus- Aaw32859 Protectin	Aaw32851 Protectin Aaw31139 Thrombus-	Aaw52391 Beta-turn Aaw52392 Beta-turn	Aaw75467 Mammalian Aay09588 Antimicro	Aay09589 Antimicro Aaw92901 Fibrinoge	Fibrinog	Aawyzyoo Fibrinoge Aay33405 Thrombin Aab10630 Oligopept	9 6										diagnosis.						
4 2 AAW94617 4 7 AAC29624 4 7 ADC22266 4 7 ADC15592		~ W 4 0		0 0 0	0 0	0 0	200	0 0 0	777	N N 0	N (V	01 N	010			ALIGNMENTS			ptide; 4 AA.				entry)	ide of desAA-fibrin.	tivator; fibrinolysis; assay;				86WO-SE000144.	85SE-00001614.	
26 19 76.0 27 19 76.0 28 19 76.0 29 19 76.0	19 76.	19 /6. 18 72. 18 72. 18 72.	18 72. 18 72. 18 72. 18 72.	18 72. 18 72. 18 72.	18 72.	18 72.	18 72. 18 72. 18 72.	18 72.	18 72.	18 72.	18 72.	18 72. 18 72.	18 72.	18 72.	18 72.			RESULT 1	AAP61324 ID AAP61324 standard; peptide; xx	AC AAP61324;	24-OCT-2003	DT 27-AUG-2003 (revised)	22-JUL-1991 (first	AA DE Sequence of tetrapeptide	XX Tissue plasminogen activator;	OS Coelognathus radiatus OS Bothrops: genus".	WO8605814-	XX PD 09-OCT-1986.	27-MAR-1986;	XX PR 01-APR-1985; 85SE-0 XX	PA (BIOP-) BIOPOOL AB. PA (RANB/) RANBY M G.
		Seconds () updates/sec	, ,	·					-						have a ng printed,				1pcion 	15320 Anti-coag	796 Sequence	861 Thrombin 198 GPRP-pept	568 Synthetic	431 laryecing 073 Sequence 677 Fibrin no	032 Non-cross 378 Cell diff	922 Fibrin po 589 Targeting	927 Acylated 381 Glycoprot	561 Oligopept 154 Targeting	227 Fibrin po 861 Anti-coag	5039 MMF subst 5860 Anti-coag 1664 Ovolin te	1005 Peptidase 1018 Hirutonin
version 5.1.6 - 2004 Compugen Ltd.	w model	19:21:01; Search time 52 S (without alignments) 21.734 Million cell		0.5	505 residues	en parameters: 15518			summaries						results predicted by chance to have to the score of the result being of the total goars distribution	פרמז פרטוב	SUMMARIES								11037 11032 Aay31032 12378 Aay32378						AAR80056 AAR80 AAW51018 Aaw51
GenCore .Copyright (c) 1993	protein search, using sw	September 7, 2004, 3	US-09-931-009A-2 : 25 1 GPRP 4	: BLOSUM62 Gapop 10.0 , Gapext (1586107 seqs, 282547505	of hits satisfying chosen	z length: 0 z length: 4	••	65	∢'⋅				7: geneseqp2003bs:* 8: geneseqp2004s:*	is the number of sater than or equa	of analysis of	ale a	Query	100.0 4 1	100.0 4 2	100.0	100.0 4 2	100.0	1000.0	100.0	100.0 4 3	100.0 4 4 100.0 4 5	100.0	88.0 4 2	0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	76.0 4 2
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Synthetic peptides beginning with the sequence Gly-Pro-Arg (e.g. GPRP) will bind to fibrinogen and prevent fibrin polymerisation. A scrambling traction was used to determine whether unique GPR-like peptides could be created from a reaction seeded with GPR and if these new products could bind to fibrinogen. See e.g. AAR32379. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying peptide(s) which bond to predetermined targets - by random degradation and recombination of peptide(s) and isolating bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                             platelet aggregation, fibrinogen A-alpha chain, protein scrambling,
GPR-like peptide.
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100.0%; Score 25; DB 2; I
llarity 100.0%; Pred. No. 1.4e+06;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                          AAR32382 standard; peptide; 4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Le
                                                                                                                                                                                                                                                                                                               Fibrinogen binding peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92WO-US006933.
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(first entry)
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-093932/11
   Query Match
Best Local Similarity
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23-AUG-1994
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01-JUL-1993
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PN field.)
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                                                                                                                                                                        The patentors claim a compsn. in which AAP61324 is pref. present at a conc. of equal to or more than, 0.4 (pref. 2) mg./ml. of the compsn. compsn. can be used in diagnostic tests such as the determn. of the enzyme tissue plasminogen activator as a standard in the detection of trace amts. of fibrin in biological fluids. It may also be administered in vivo to measure the total fibrinolyric capacity of an organism. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 27-400-2003 to correct OS field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                       Fibrin solubilised with tetra:peptide - used in diagnostic procedures for determining fibrinolysis factors.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide contg. proline - is used for cerebral thrombosis, myocardial infarction etc. due to anti-coagulation activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal is in amide form. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-coagulant; cerebral thrombosis; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                      Length 4;
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Pred. No. 1.4e+06;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= ornithine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR05320 standard; peptide; 4 AA
                                                                                                                                                                                                                                                                                                                                                                    100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                            Claim 2; Page 18; 22pp; English
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-coagulant peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1990-175285/23.
                                                      WPI; 1986-278827/42.
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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Misc-difference
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08-OCT-1990
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                         Ranby M;
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The inventors claim a method for inexpensively and rapidly producing a large and varied population of peptides and screening this varied population for the presence of peptides which bind to a target, for example, a macromolecule associated with a particular physiological function. The specific binding peptides are isolated and sequenced, synthesised on a large-scale, their biological activity is demonstrated, and then subjected to clinical testing. The random population of peptides is generated by employing a scrambling system which utilises one or more proteins esp. papain, pepsin, bromelin, thermolysin, trypsin, pronase, chymctrypsin, subtilism and dipeptidyl peptidase IV. A typical starting processes, partic. fibrinogen, sickle cell haemoglobin, collagenase IV, remain; Gp. IIb IIIa or phospholipase A2. It has been demonstrated that synthetic peptides beginning with the sequence GPR will bind to fibrinogen. Such peptides include GPR, GPRP and GPRV. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                          Identifying peptides which binds to a specific target - by contacting target with scrambled equilibrium mixt. of many peptide derived from protein by incubation with protease, for detecting potential therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombin; inhibitor; aggregation; platelet; determination; assay; qualitative; quantitative; fibrin.
                Random degradation; recombination; scrambling reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW09861 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                         Example; Page 54; 97pp; English
                                                                                                                                         93WO-US008231
                                                                                                                                                                     92US-00932200
                                                                                                                                                                                                                                 Hopfinger AJ;
                                                                                                                                                                                                (RECE-) RECEPTOR LAB INC.
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Best Local Similarity
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                                                                           WO9404558-A1
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                                             Synthetic.
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In the qualitative or quantitative determn. Of thrombin-induced platelet aggregation in the presence of fibrin, interference from fibrin clot formation is suppressed with a fibrin-aggregation inhibitor (e.g. AAM09861-63). The assay may be used to determine the platelet aggregation inhibitory activity of thrombin inhibitors. The peptides inhibit fibrin clot formation at high thrombin concns. without inhibiting platelet
                                                                                                                                 Determn. of thrombin-induced platelet aggregation in presence of fibrin comprises use of fibrin aggregation inhibitor to suppress fibrin clot formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPRP, glycine, proline, arginine, proline, bladder irrigation, cell adhesion molecule, binding, tumour removal, endoscopic operation, transurethral resection, cancer, neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW25198 and AAW25199 are peptides containing a GPRP sequence. The peptides are capable of binding to cell adhesion molecules and are uin aqueous irrigation solutions for use during and after endoscopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ic irrigation solns. - contg. peptide(s) that bind to cell molecules.
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW25198 standard; peptide; 4 AA.
 94EP-00119803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95DE-01029909
                                                                                                                                                                                                Claim 4; Col 5; 5pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                       (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FREP ) FRESENIUS AG.
                                                                                                              WPI; 1995-233339/31.
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Best Local Similarity
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15-DEC-1994;
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                                                                                                                                                                                                                                                                                                             aggregation
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                                                                                 Reers M;
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AAW25198
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Gaps

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Length 4; 0; Indels

100.0%; Score 25; DB 2; I 100.0%; Pred. No. 1.4e+06; Mismatches

0;

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tripeptide, Gly-Pro-Arg is also claimed. This tripeptide sequence tripeptide, Gly-Pro-Arg is also claimed. This tripeptide sequence tripeptide, Gly-Pro-Arg is also claimed. This tripeptide sequence trooperated to the first 3 amino acids of the alpha-chain exposed by the thrombin catalysed release of the fibrinopeptide A in all vetebrate species. In the present peptide, the addition of a proline residue at postion 4 increases the affinity of the peptide for fibrinosen almost tenfold. These synthetic fibrinogen binding peptides are immobilised on a novel polysaccharide support (e.g. Sephadex), to which they are coupled through a spacer or linker moiety. This linker moiety comprises a chain of greater then 7 atoms. The solid support is useful for the recovery and isolation of fibrinogen from material such as plasma, plasma fractions and fibrinogen—containing cell culture media arising from the production other known affinity isolation procedures. The process is superior to other known affinity isolation procedures in that only mild elution by buffers are required to recover the bound fibrinogen.
operations. Preferred irrigation solutions are electrolyte-free and contain I microgofmit to 100 mg/ml of one or more oligopeptides containing the amino acid sequences: RGD, LDV, LDA, DGRA, GRRP, VTL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid code). The solutions are especially used for irrigating the bladder during and after tumour removal by transurethral resection. The peptides protect against recurrence of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibrinogen binding peptide; fibrinopeptide A; fibrinogen isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recovery of fibrinogen using polysaccharide solid support coupled fibrinogen-binding peptide - requires only mild elution buffers.
                                                                                                                                                                                                                              ö
                                                                                                                                                                                        Length 4;
                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                      Score 25; DB 2; L
Pred. No. 1.4e+06;
                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic fibrinogen binding peptide 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goss N;
                                                                                                                                                                                                                                                                                                                                                                                                AAW34568 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 14; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oates A,
                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-AU000013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96AU-00007564
                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pham H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-385298/35
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CSLC-) CSL LTD.
                                                                                                                                                                                                                                                                 1 GPRP 4
                                                                                                                                                                                                                                                                                                     1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4 AA;
                                                                                                                                                    Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9726280-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kanellos J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                              Matches
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This sequence represents a targeting ligand directed to the GPIIDIIIa receptor. The invention relates to a concrast agent for diagnostic imaging or a target composition which comprises: (i) a lipid, protein or polymer and (ii) a gas, in combination with (iii) a targeting ligand (TI). Ti targets calls or receptors selected from myocardial, endothelial, epithelial and tumnour cells and the glycoprotein GPIIDIIIa receptor. Also claimed are: a composition comprising vesicles containing (i) - (iii) and an aqueous carrier; a targeted vesicle composition comprising a fluorinated gas and a targeting ligand (TI) which targets tissues or receptors; a formulation for therapoutic or diagnostic use comprising (i)-(iii) and a bloactive agent; and a method for providing in mage of an internal region of a patient, or for diagnostic the presence of diseased tissue, comprising (a) administration of a composition as above; and (b) scanning the patient using ultrasound to obtain a visible image of the region or diseased tissue. The methods and compounds are cospering in the indial patient using ultrasound to obtain a visible image of the region or diagnosing the presence of diseased tissue, ceppecially myocardial, endothalial or epithelial tissue but also gastrointestinal and cardiovascular regions. In particular the ligand trangers regions of arteriosclerosis. Stabilised vesicles are particularly useful for nerfusion in the vesicle as a particularly useful for nerfusion in the vesicle as a particularly useful for nerfusion in the vesicle as a particularly useful for nerfusion in the vesicle as a particularly useful for nerfusion in the vesicle as a particularly useful for nerfusion in the vesicle as a particularly useful for nerfusion in the vesicle as a particular vesicle as a particular vesicle and composition in the vesicle as a particular or epithelial vesicle as a particular vesicle as a particular vesicle as a particular vesicle and composition and arteriors or a vesicle as a particular vesicle as a particular vesicle and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for perfusion imaging. The vesicles may also be used to deliver active agents to an intended target such as tissue or a receptor, and ilrasound can then be used to promote rupture of the vesicles and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contrast agent or targeted compsn. for imaging or treating diseased tissue - comprising lipid, protein or polymer, a gas, and a targeting ligand e.g. a protein, peptide, saccharide or steroid.
                                                                                                                                                                                                                                                                                                                               Targeting ligand directed to the glycoprotein GPIIb/IIIa receptor.
                                                                                                                                                                                                                                                                                                                                                                              Contrast agent, targeted composition, diagnosis, diseased tissue, glycoprotein GPIIb/IIIa receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ultrasound can then be used to promote rupture of release a bioactive or diagnostic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 2; L
llarity 100.0%; Pred. No. 1.4e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 55; 175pp; English.
                                                                                                                                                                             AAW45491 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US009938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00497684.
96US-00640464.
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMAR-) IMARX PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-077233/07.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4 AA;
1 GPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9640285-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
01-MAY-1996;
                                                                                                                                                                                                                                                                                20-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unger EC,
                                                                                                                                                                                                                            AAW45491;
                                                                                                                                                       AAW45491
                                                                                                                           RESULT
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Gaps

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Indels

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Gaps

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Query Match

100.0%; Score 25; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.46+06;
Matches 4; Conservative 0; Mismatches 0; Indels

99WO-EP001599.

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New assays for determination of activity of components in the Protein C anticoagulant pathway, used for the study of diseases such as deep venous thrombosis and pulmonary embolism.
                         Fibrin polymerisation inhibitor; factor Xa; thrombin; factor VIII; factor X; cosgulation factor; blood; photometric; frotein C anticoagulant pathway; thromboembolic disease; deep venous thrombosis; pulmonary embolism.
  Fibrin polymerisation inhibitor peptide
                                                                                                                                                                                                            (CHRO-) CHROMOGENIX AB
                                                                                                                                                                                                                                     Rosen BS, Hall CMY;
                                                                                                                                                                                                                                                           WPI; 1999-571846/48.
                                                                                                              WO9947699-A1.
                                                                                                                                                              11-MAR-1999;
                                                                                                                                                                                     .9-MAR-1998;
                                                                                                                                      3-SEP-1999
                                                                                        Synthetic.
   The invention relates to new thrombolytic agents which comprise a thrombolytic proteinase covalently linked to a targeting compound capable of specifically binding to a component of a thrombol. The thrombolytic agents can be used for elaminating thrombi in vivo in, e.g. myocardial infarction, cerebral ischaemia, deep vein thrombosis or pulmonary image thrombolytic agent can also be used to specifically targeted to thrombolytic agent can also be used to specifically targeted to thrombol sites in vivo and have minimal amemorrhapic side effects and side effects related to non-specific proteolysis. Multiple copies of the present amino acid sequence (GPRP) may be used in a fibrin-specific targeting compound. (Updated on 25-MAR-2003 to correct PI field.)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                         New thrombolytic agents - comprise thrombolytic proteinase covalently linked to targetting compound for binding to component of thrombus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                          Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 25; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                   Sequence contained in fibrin-specific targeting compound.
                                                                                                                                                                                                                                                                                                                                                                                             Swenson S, Flores Sanchez
                                                                                 AAW52073 standard; peptide; 4 AA
                                                                                                                                                                                                                                                                                                                                                      (DIAT-) DIATIDE INC.
(UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 63; 79pp; English.
                                                                                                                                                                                                                                                                                                        97WO-US021918
                                                                                                                                                                                                                                                                                                                              96US-00753781
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Bush LR,
                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-333336/29.
              GPRP
 GPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Markland FS,
                                                                                                                                                                                                                                                                                                                                02-DEC-1996;
                                                                                                                                                                                                                                                      WO9824917-A1
                                                                                                                                                                                                                                                                                                       02-DEC-1997;
                                                                                                                                25-MAR-2003
23-SEP-1998
                                                                                                                                                                                                                                                                                11-JUN-1998
                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                        thrombus.
                                                                                                        AAW52073,
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Assays have been developed for the determination of activity of components in the Protein C anticoagulant pathway using additional metal ions to improve the sensitivity of the assays. An in vitro photcometric method for qualitative screening and quantitative determination of the functional activity of components of the Protein C anticoagulant pathway of body coagulation, comprises measuring the conversion rate of an exogenous substrate by an enzyme. The activity of the enzyme is related to the Protein C anticoagulant activity, in a blood sample of a human of coagulation factors and the exogenous substrate after at least partial activation of coagulation through the intrinsic, extrinsic, or partial activation of coagulation py: (1) adding calcium ions; common pathway and triggering coagulation by: (1) adding calcium ions; common pathway and triggering coagulation by: (1) adding calcium ions; common pathway and triggering coagulation by: (1) adding calcium ions; adding further metal(s) ions selected from divalent metal ions and coagulation, for determination of free Protein C anticoagulant pathway of blood coagulation, for determination of free Protein S activity in a blood sample, coagulation, for determination of free Protein C activity in a blood sample, coagulation and diagnosing of defects in the Protein C activity in a blood sample, coagulation and diagnosing of defects in the Protein C activity in a blood sample, coagulate pathway in investigation of patients with thromboembolic diseases such as deep venous thromboens and/or pulmonary embolism. The present sequence represents a fibrin polymerication inhibitor for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h Similarity 100.0%; Score 25; DB 2; Length 4; Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Indels
Claim 27; Page 50; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY31032 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY31032;
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PAY41677 standard; peptide; 4 AA.

RESULT 10

GPRP 4

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1 GPRP

(first entry)

07-DEC-1999

AAY41677;

AAY41677 ID AAY4 XX AC AAY4 XX DT 07-I

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Cell differentiation; cell proliferation; cell maintenance; ectoderm-like cell; embryonic stem cell; pluripotent cell; gene therapy; cell therapy; tissue transplant; organ transplant; xerotransplant; allotransplant; concomitant transplantation; transgenic animal.
                                                                                                                                                                                  Example 22; Col 83-84; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  AAY32378 standard; peptide; 4 AA.
                                                                                       91US-00641720.
92US-00959560.
93US-00069831.
                                                                          96US-00747137.
                                                                                                            94US-00212546
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                           (HEMO-) HEMOSPHERE INC
                                                                                                                                                       WPI; 1999-508153/42.
                                                                                                                                                                                                                                                                                                                                                 1 GPRP 4
                                                                                                                                                                                                                                                                                                        Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9953021-A1
                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000
                                                                          12-NOV-1996;
                                                                                        15-JAN-1991;
13-OCT-1992;
                                                                                                             14-MAR-1994;
                                               US5945033-A
                                                             31-AUG-1999
                                                                                                      01-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                AAY32378;
                                                                                                                                         (en RCK;
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This sequence represents a peptide that can form the low mol.wt.

Component of a novel biologically active factor that is capable of
influencing the differentiation, proliferation and/or maintenance of
component cells. The factor consists of a low mol.wt. component
selected from Pro. Pro-Ala, Ala-Pro-Gly, Pro-OH-Pro, Pro-Gly, Gly-Pro-
CC Ala, Gly-Pro-OH-Pro, a peptide given in AAY32378-82, or a protease
cd digested (including collagenase digested) collagen fragment, and a high
cmol.wt. component such as fibronectin. The biologically active factor is
cobtained from conditioned media of hepatic or hepatoma cells or cell
consisted active factor is
capable of causing the transition of pluripotent cells (e.g. embryonic
capable of causing the transition of pluripotent cells (e.g. embryonic
cells having different properties, more specifically primitive ectoderm-
cclls (EDP) cells. The factor is also capable of maintaining and
supporting proliferation of these cells in vitro. It also allows the
collation and maintenance of EDL cells derived from in vitro and in vivo
primitive eccoderm. These cells can be used from in vitro and in vivo
creplacement, and gene therapy. They can also be used for producing
chimeric or transgenic animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m; GPIIb/IIIa receptor; cyclic peptide ligand.
                                                                                                                                                                                                                                                                                               New isolated biologically active factor capable of influencing differentiation, proliferation or maintenance of pluripotent cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 3; Length 4; 100.0%; Pred. No. 1.4e+06; ive . 0; Mismatches 0; Indels
                                                                                                                                                                                                         Rathjen J;
                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 122; 189pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY54922 standard; peptide; 4 AA.
                                              99WO-AU000265.
                                                                                           98AU-00002912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibrin polymerisation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rathjen PD,
                                                                                                                                                                  (BRES-) BRESAGEN LTD.
                                                                                                                                                                                                                                                      WPI; 2000-061970/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4 AA;
                                                                                             09-APR-1998;
23-SEP-1998;
                                                 09-APR-1999;
21-OCT-1999.
                                                                                                                                                                                                              Bettess MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel aqueous suspension of monodisperse table against dissolving upon dilution with an alcohol-free aqueous stable against dissolving upon dilution with an alcohol-free aqueous medium. The method involves (a) forming an aqueous solution containing albumin and hemoglobin and (b) treating the aqueous solution ontaining alcohol to cause the solution to become turbid. The particles are useful as agents for in vivo administration, either of their own administration or as a vehicle for other therapeutic or diagnostic agents. The method permits the formation of albumin and hemoglobin particles in the method nanometer and micrometer size range, in a form closer to their natural form than the forms of the prior art. The particles therefore constitute amore closely controlled agent for in vivo administration, with greater ease of clearance from the body after their period of usefulness.

ANY30952-Y31135 represent peptides used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-crosslinked protein particles for therapeutic and diagnostic use.
                                                 Non-crosslinked protein particle; diagnostic; therapy; monodisperse; albumin; haemoglobin; nanometer; micrometer; clearance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell differentiation, proliferation and maintenance factor peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 25; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
         Non-crosslinked protein particle peptide 81.
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0; Gaps

95US-00484773. 92US-00886052.

07-JUN-1995; 21-MAY-1992; 11-JUL-1994;

US5968476-A.

19-OCT-1999

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A complex used for thrombus imaging comprises technetium-99m complexed with a peptide ligand for {\tt GPIIb/IIIa} receptor.
                  Lister-James J;
      (DIAT-) DIATIDE INC
                             WPI; 2000-021733/02
                 RT,
                  Dean
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This sequence represents the fibrin polymerisation site. The invention relates to a complex (A) for thrombus imaging comprises technetium-99m (Tc-99m) completed with a reagent comprising a peptide (P) with 4 to 100 amino acids sequence and a Tc-99m binding moiety covalently bound to (P). (P) is selected from a linear peptide ligand for a GPIDIATIA receptor not comprising the amino acid sequence (arginine-glycine-aspartate) a peptide ligand for a polymerisation site of fibrin, and a cyclic peptide ligand for the GPIDATIA receptor. The thrombus imaging reagents provided by the present invention can be used for visualising thrombi in a mammalian body when Tc-99m is labelled Claim 7; Col 31-32; 18pp; English Sequence 4 AA;

Gaps ; 0 h Similarity 100.0%; Score 25; DB 3; Length 4; Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches

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|||| 1 GPRP 4 1 GPRP 4

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AAB20589 standard; peptide; 4 AA. RESULT 14 AAB20589

12-DEC-2000 (first entry) AAB20589;

Targeting ligand peptide #5.

Targeting ligand peptide; imaging; ultrasound; vesicle; tumour; myocardial; endothelial; epithelial; glycoprotein GPIDbILIa receptor; detection; thrombus; integrin; malignancy; inflammation; lesion; atherosclerotic plaque; carcinoma.

Synthetic

WO200045856-A2

10-AUG-2000

02-FEB-2000; 2000WO-US002620.

(IMAR-) IMARX PHARM CORP.

Wu Y; Ungr EC, WPI; 2000-532867/48.

Ultrasound method, useful for diagnosis of e.g. thrombi or carcinomas, uses different types of energy for priming and interrogating the subject.

Disclosure; Page 68; 211pp; English.

The present invention describes an ultrasound method comprising: (i) administering a targeted vesicle composition $(A)_i$ and (ii) scanning the subject by exposure to a first type of ultrasound energy and then

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New protected amino-substituted compounds bearing acylated N-methyl-alpha aminoisobutyryl moiety as amino protecting group, useful e.g. in organic synthesis and in the formulation/delivery of prodrugs with improved bloavailability.
interrogating with a second type of ultrasound energy. (A) consists of a combination a lipid, protein or polymer, encapsulating a gas, in combination with a targeting ligand. The method is used to detect: (I) a thrombus (particularly old or echogenic); (II) a low concentration of vesicles; or (III) vesicles targeted to endothelial tissue, particularly those containing integrins associated with malignancy or inflammation in early or small lesions, e.g. atherosclerotic plaque or ovarian, microbubbles and reduces background noise. The present sequence represents a targeting ligand peptide which is used in the method of the present invention
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acylated amino protection; chemical synthesis; drug delivery; bioavailability; biostability.
                                                                                                                                                                                                           100.0%; Score 25; DB 3; Length 4; 100.0%; Pred. No. 1.4e+06; Attive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acylated amino protecting method fibrinogen peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYCA-) UNIV CALIFORNIA SAN DIEGO.
                                                                                                                                                                                                                                                                                                                                                                            AAB98927 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-2000; 2000WO-US040671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-1999; 99US-0157435P.
30-JUN-2000; 2000US-00609565.
                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2001 (first entry)
                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Creighton CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-389649/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200125170-A1.
                                                                                                                                                                                Sequence 4 AA;
                                                                                                                                                                                                                                                                       1 GPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         AAB98927;
                                                                                                                                                                                                                                                                                                                                              RESULT 15
AAB98927
      8,888888888888
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The present invention describes protected amino-substituted compounds with an acylated N-methyl-alpha-aminoisobutyryl (NMeAib) moiety as the amino protecting group. These can be used in chemical synthesis and in drug delivery. They can be used as prodrugs which have improved biostability or bioavailability. The present sequence is a peptide described in the exemplification of the invention Length 4; Sequence 4 AA;

Disclosure; Page 12; 39pp; English.

ö Gaps . 100.0%; Score 25; DB 4; L llarity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 4; Conserv

13.

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ABG74561 standard; peptide; 4 AA.

RESULT 17

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This invention relates to a novel targeted compound having a combination of hydrophobic compound, hydrophilic polymer and targeting ligand. The invention also comprises a target vesicle composition comprising ligand. The protein or polymer gas filled vesicles in an aqueous carrier, a method for imaging a thrombus in a region of a patient involving administering to the patient a target vehicle composition and scanning the region (preferably cardiac region) with diagnostic imaging a thrombus in a blood or internal region of a patient which can be used to obtain a visible image of a region (preferably arteriosclerosis, atherosclerotic plaque, infarcted myocardium or a cancer cell) and a method for diagnosing the presence of disease tissue in a patient involving administering a target vehicle composition and scanning the patient using ultrasound to obtain a visible image of the region. The methods of the invention may be used for inaging a thrombus in a region of a patient, lysing a thrombus in a blood vessel, diagnosing the presence of diseased tissue in a patient and for the the therapeutic delivery in vivo of a bioactive agent. The compounds of the invention are easily synthesised and have diagnostic efficacy, art methods when represents a farceting lor the the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New targeted compound useful in target vesicle composition for imaging a thrombus in a region of a patient has a combination of hydrophobic compound, hydrophilic polymer and targeting ligand.
                                                                                                                                                                                                                                                                                                                               Target vesicle; diagnostic imaging; thrombus; cancer; arteriosclerosis; atherosclerotic plaque; infarcted myocardium; glycoprotein GPIIbIIIa receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   art methods. The present sequence represents a targeting ligand to the glycoprotein GPIIbIIIa receptor used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 5; Length 4; llarity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             Glycoprotein GpIIbIIIa receptor targeting ligand #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schumann PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 65; 206pp; English.
                                                                                                                                                         ABG30381 standard; peptide; 4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMAR-) IMARX THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2001; 2001WO-US032308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-2000; 2000US-00699679
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-489986/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40200236161-A2.
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                                                                                                                                                                                                                                               07-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unger EC,
                                                                                                                                                                                                  ABG30381;
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Matches
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This invention describes a novel DNA construct encoding a polypeptide comprising several oligopeptide units and including recognition sites for peptide cleavage. The products of the invention have cytostatic and antibacterial activity, inhibit tumour cell adhesion and can be used to prepare vaccines. The constructs are used for recombinant production of peptides used, in a rinse solution, to reduce the high rate of relapse in superficial bladder carcinoma after transurethral resection or as antimicrobial peptides for control of antibiotic-resistant bacteria in human or veterinary medicine. The constructs allow the possible concentration and reduced cost. This sequence represents an oligopeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          New DNA construct encoding polypeptide that includes cleavage sites, useful for preparation of pharmaceutical peptides or their mixtures.
                                                                                         Cytostatic, antibacterial, tumour cell adhesion inhibitor, vaccine, bladder carcinoma, transurethral resection, antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Targeting ligand #4 used in novel diagnostic ultrasound method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h Similarity 100.0%; Score 25; DB 6; Length 4; Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   Volker L;
                                                                                                                                                                                                                                                                                                                                                   Sommermeyer K,
                                                                                                                           human medicine; veterinary medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU63154 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 3; 12pp; German.
                                                                                                                                                                                                                                                                                                                   (FREP ) FRESENIUS KABI DEUT GMBH
                                                                                                                                                                                                                                                      14-MAY-2001; 2001DE-01023348.
                                                                                                                                                                                                                                                                                  14-MAY-2001; 2001DE-01023348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-2003 (first entry)
                                                            Oligopeptide fragment #2.
                                                                                                                                                                                                                                                                                                                                                   Eichner W,
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-168758/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4 AA;
                                                                                                                                                                                         DE10123348-A1.
                                                                                                                                                           Unidentified
                            24-APR-2003
                                                                                                                                                                                                                       21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                   Dormann D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU63154;
ABG74561;
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Ultrasound method; targeted vesicle composition; targeting ligand;

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Gaps ; 0

1 GPRP 4

antirheumatic; antiinflammatory; antiarthritic; peptide therapy; proinflammatory; tetrapeptide; inflammation; synovial joint inflammation; rheumatoid arthritis; fibrinogen A alpha chain; fibrin polymerisation;

Fibrin polymerisation inhibiting peptide seq id 2.

L5-JAN-2004 (first entry)

ADD32227;

ADD32227 standard; peptide; 4 AA.

ADD32227

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Ultrasound diagnosis, by administering targeted vesicle composition with vesicles encapsulating gas, in combination with targeting ligand, to a patient, and scanning patient by dual frequency ultrasound insonation.
        liposome; phospholipid; ultrasound energy; vesicle oscillation; reflected ultrasound signal; ultrasound diagnosis; echogenic thrombus; endothelial tissue; apithelial cell; tumour cell; myocardial cell; integrin; malignancy; inflammation; heart; diseased tissue; imaging; gastrointestinal region; lymphatic system.
ultrasound scanning; dual frequency ultrasound insonation; micelle;
                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB MEDICAL IMAGING INC.
                                                                                                                                                                                                                                                                                                              Disclosure; Col 49; 96pp; English
                                                                                                                                                          96US-00640464.
96US-00660032.
98US-0073913P.
                                                                                                                              99US-00243640
                                                                                                                                                                                        98US-00218660
                                                                                                                                                                                                                                                  WPI; 2003-531036/50
                                                                                                                                                                                                                               Unger EC, Wu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4 AA;
                                                                                       US6521211-B1
                                                                                                                                                           01-MAY-1996;
                                                                                                                                                                               06-FEB-1998;
22-DEC-1998;
                                                                                                                              03-FEB-1999;
                                                                                                                                                 07-JUN-1995
                                                                                                           18-FEB-2003
                                                                     Synthetic.
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Inducing proinflammatory effects in human synovial or fibroblast cells comprises using a specific tetrapeptide which can also identify a receptor to the tetrapeptide.

WPI; 2003-829401/77.

(SMIT/) SMITH T H.

Smith TH;

17-AUG-2001; 2001US-00931009. 17-AUG-2001; 2001US-00931009.

US2003109431-A1.

12-JUN-2003

Homo sapiens.

Synthetic

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The present invention relates to a novel ultrasound method which involves administering to a patient a targeted vesicle composition which comprises commissionable and as a combination with a targeting ligand, and scanning the patient using dual frequency ultrasound insonation. The canning the patient using dual frequency ultrasound insonation. The vesicles themselves comprise a lipid, protein or polymer, and are to phospholipid selected from diolecylphosphatidylcholine, dipalmitoylphosphatidylcholine, distance, dipalmitoylphosphatidylcholine, distance, dipalmitoylphosphatidylcholine, distance, dipalmitoylphosphatidylcholine, distance, dis
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100.0%; Score 25; DB 7; Length 4; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
  Query Match
Best Local Similarity
Matches 4; Conserv
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1 GPRP 4

RESULT 19

4; Conservative

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The invention describes a method of inducing proinflammatory effects in synovial or fibroblast cells comprising exposing the cells to a specific tetrapeptide (GRRP) peptide (I). (I) is used for inducing proinflammatory effects in synovial or fibroblast cells. An analogue of (I) is used for treating or preventing inflammation of a synovial joint or rheumatoid arthrits in a subject. (I) is used to identify a receptor for (I) comprising exposing several fibroblastic cells or synovial cells to (I). (I) Can identify, isolate and clone the cell receptor to which it binds. This is the amino acid sequence of a fibrin polymerisation inhibiting peptide derived from the human fibrinogen A alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity 100.0%; Score 25; DB 7; Length 4; Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR05861 standard; protein; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-coagulant peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4 AA;
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08-OCT-1990
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DT 25-M
DT 08-O
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The present invention describes an isolated matrix metalloproteinase-2 (MPMP-2), MPMP-9 or MT1-MMP selective substrate polypeptide (I), or its functional peptidominetic. Also described is a method for preferentially directing a moiety to a site of MMP-2, MMP-9 or MT1-MMP activity. By administering (I) to the subject. (I) have cytostatic, antiinflammatory and neuroprotective activities, and can be used in gene therapy. The polypeptides and methods from the present invention can be used for heurodegenerative diseases. Asstaglogenesis, inflammatory or neurodegenerative diseases. Asstaglogenesis, inflammatory or neurodegenerative diseases. Asstaglogenesis in the exemplification of the present invention
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide contg. proline - is used for cerebral thrombosis, myocardial infarction etc. due to anti-coagulation activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal is in amide form. (Updated on 25-MAR-2003 to correct
field.)
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                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                               h Similarity 100.0%; Score 19; DB 6; Length 3; Similarity 100.0%; Pred. No. 1.4e+06; 3; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= proline or prolylproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= ornithine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 975; 10pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR05860 standard; protein; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-coagulant peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1990-175285/23.
                                                                                                                                                                                                                                                              Local Similarity
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Misc-difference
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                                                                                                                                                                                                                                                                                                                     2 PRP 4
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                                                                                                                                                                                                                                                                                                                                                         1 PRP 3
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08-OCT-1990
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                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR05860
X88888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated matrix metalloproteinase-2 (MMP-2), MMP-9, MTI-MMP selective substrate polypeptide, useful for diagnosing and treating tumor angiogenesis, inflammatory or neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matrix metalloproteinase; MMP-2; MMP-9; MT1-MMP; substrate; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptidomimetic; antiinflammatory; neuroprotective; gene therapy;
tumour angiogenesis; inflammatory disease; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                      Peptide contg. proline - is used for cerebral thrombosis, myocardial infarction etc. due to anti-coagulation activity.
                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminal is in amide form. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 2; Length 4; Pred. No. 1.4e+06; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMP substrate cleavage related peptide SEQ ID NO:101.
                                                                                 /label= proline or prolylproline.
     Location/Qualifiers
3
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                                                 'label= ornithine.
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 975; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR55099 standard; peptide; 3 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2002; 2002WO-US029060.
                                                                                                                                                                                             88JP-00265809
                                                                                                                                                                                                                              88JP-00265809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2001; 2001US-00953592.
                                                                                                                                                                                                                                                                  (DAUC ) DAIICHI SEIYAKU CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-354595/33.
                                                                                                                                                                                                                                                                                                    WPI; 1990-175285/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen EI,
                                Misc-difference
                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPRP 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4 AA;
                                                                                                                                                                                            21-OCT-1988;
                                                                                                                                                                                                                                21-OCT-1988;
                                                                                                                       JP02115197-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR55099;
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RESULT 23

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                                                                                                                       140 kDa peptidase hydrolyses proline rich proteins - useful for prevention and treatment of diseases related to proline rich proteins and
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                                                                                                                                                                                                                        The sequences represented by AAR80046 and AAR80048-R80059 are substrates for the novel peptidase of the invention. The peptidase hydrolyses P-P-P-P-P-A- and P-P-B and recognises the proline at the second residue from the N-terminal of a peptida to release the N-terminal amino acid. The enzyme's activity is stimulated with Mnc12 and inhibited with ophenanthroline and 2-mercaptoethanol. The peptidase is useful for the hydrolysis of proline containing physiologically active peptides, oligoproline and proline rich proteins in the living body, particularly in the brain of mammals. The peptidase is useful for the present of proline rich proteins and treatment of proline rich protein related diseases and study of cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thrombin inhibitor useful for inhibition of thrombin-mediated functions comprises a means for inactivating or sequestering thrombin and portion of fibrinogen chain that binds at the anion-binding exosite of thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/note= "D-form residue, N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hirutonin-2, a thrombin catalytic site inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY. (NIHA-) NIPPON HAM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%; Score 19;
100.0%; Pred. No.
ive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                          Example 4; Page 6; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW51018 standard; peptide; 4 AA.
                                                                                                                                                          studies of cerebral functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US010429
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94JP-00042027
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                                                                                     WPI; 1995-331519/43.
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PRP 3
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Modified-site
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   15-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                           functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW51018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The peptide is useful for treatment of tumours, infections caused by virus, bacteria or fungi, or autoimmune disease. It can be administered orally or parenterally at daily dose of 1-500 mg (p.o.) for adults. The cyclisation is effected with a condensing agent in a solvent opt. in the presence of a base at -50 degrees C to 50 degrees C for 30 minutes to 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumours, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                               Infection; virus; bacteria; fungi; autoimmune disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o-phenanthroline; 2-mercaptoethanol; oligoproline;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cyclic tetra:peptide(s) useful for treatment of tumou prepd. by cyclisation reaction with condensing agent e.g. di:cyclo:hexyl:carbodiimide in presence of base.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.0%; Score 19; DB 2; Length 4; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                               for tumour treatment (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR80056 standard; peptide; 4 AA.
                                                                        AAR21664 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 1; 12pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
                                                                                                                                           (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptidase substrate #10
                                                                                                                                                                               Cyclic tetrapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-076791/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptidase; o-phene
cerebral function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4 AA;
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                                                                                                                                                                                                                                                                                                                                                         11-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1990;
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                                                                                                                                           17-JUN-1992
                                                                                                                                                                                                                                                                                                                     24-JAN-1992,
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                                                                                                                                                                                                                                                  Synthetic.
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RESULT 24

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The invention relates to a new thrombin inhibitor which comprises: (a) a means for inactivating or sequestering thrombin, and (b) a portion of the fibrinogen gamma. Chain that binds at the anion-binding exosite of thrombin. Also claimed is a recombinant genetic construct comprising nucleic acid sequences encoding the inhibitor above. The inhibitor comprises three segments, the first binds to the catalytic site of thrombin, the second connects the first binds to the catalytic site of thrombin, the second connects the first and third segments, and the third comprises a portion of the fibrinogen gamma' chain that binds to the thrombin exosite. The third segment is preferably amino acids 414-427 of the native human fibrinogen gamma' sequence. The inhibitor is useful for the inhibition of thrombin-mediated functions in a patient or in extracorporeal blood. The present sequence represents a thrombin catalytic site inhibitor, hirutonin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spiro[Pyrrolidine-2':3-piperidin-2-ones] and their fused ring analogues used, e.g. to modulate signal transduction protein interactions, inhibit cell growth and for use in treating infections and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Src homology 3 domain; SH3 domain; peptidomimetic; mimetic; modulator; beta-turn template; spiro[pyrotlidine-2':3-piperidin-2-ones]; fused ring analogue; signal transduction protein interaction; inhibit cell growth; infection; cancer.
                                                                                                                                                                                                                                                                                                       h Similarity 100.0%; Score 19; DB 2; Length 4; Similarity 100.0%; Pred. No. 1.4e+06; 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Src homology 3 domain peptide mimetic tetrapeptide #1.
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 Disclosure, Page 7; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW94617 standard; peptide; 4 AA.
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Matches 3; Conserv
                                                                                                                                                                                                                                                                            Sequence 4 AA;
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18-MAY-1998;
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                                                                                                                                                                                                                                                                                                           Query Match
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The present invention describes spiro[Pyrrolidine-2':3-piperidin-2-ones], their fused ring analogues, and salts of both, all as individual compounds or their libraries. They are peptidonimetics, and interact with protein Src homology 3 (SH3) domains, involved in protein-protein

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Gaps ;

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interactions in signal transduction. They cause disruption of the pathway in particular, they inhibit the protein tyrosine kinase system involved in cell growth regulation. The cells may be microbial, e.g. pathoganic bacterial or fungal cells responsible for infections, or of transformed cells, e.g. responsible for neoplastic conditions. Specific examples of Src proteins with SH3 domains are those known by the abbreviations p85, Fyn, Lyn, Hck, Syk, GrD, Gap, STAT, p47-phox, p67-phox, and Brk. The present sequence represents a tetrapeptide used in a spiro[Pyrrolidine-2':3-piperidin-2-ones] of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to peptides with anti-angiogenic activity. The peptides of the invention are useful for inhibiting angiogenesis, for treating conditions that arise from, or are exacerbated by, angiogenesis such as cancer, autoimmune diseases (e.g. rheumatoid, immune and dependentive arthritis), ocular diseases (e.g. diabetic rethinopathy), skin diseases (e.g. psoriasis), blood vessel diseases (e.g. haemangiomas) crohn's disease, atherosclerosis, keloids, or ulcers, or for preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compounds with anti-angiogenic activity, useful for inhibiting angiogenesis, treating conditions that arise from, or are exacerbated angiogenesis, e.g. cancer or autoimmune diseases, or preventing metaatases from tumors.
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-angiogenic; angiogenesis; cancer; autoimmune disease; rheumatoid arthritis; immune arthritis; degenerative arthritis; occular disease; diabetic retinopathy; skin disease; boriasis; blood vessel disease; haemangioma; Crohn's disease; atherosclesosis;
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                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                             Length 4;
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAO29624 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-angiogenic peptide #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB.
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                                                                                                                                                                                          Sequence 4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 27
AAO29624
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us-09-931-009a-2.closed.rag

metastases from the tumours. The peptides are also useful as control agents, by inhibiting ovulation and establishment of for reducing bleeding. The present sequence is an example of the invention ន្តដូចនេះ

birth placenta, or peptide of

Sequence 4 AA;

ó Gaps . , DB 7; Leus. O. 1.4e+06; Indels Query Match 76.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 3; Conservative 0; Mismatches

a 8

ADC22266 standard; peptide; 4 AA. 18-DEC-2003 (first entry)

Protein binding domain amino acid sequence SEQ ID NO:115.

recombinant fusion protein; fusion protein; binding; detection; localisation domain; binding domain; subcellular compartment localisation.

Homo sapiens

WO2003012068-A2

13-FEB-2003,

01-AUG-2002; 2002WO-US024572.

01-AUG-2001; 2001US-0309395P. 13-DEC-2001; 2001US-0341589P.

(CELL-) CELLOMICS INC

Bright G, Premkumar DR,

Chen Y;

WPI; 2003-248174/24. N-PSDB; ADC22267.

New recombinant fusion protein comprising detection and first localization domains and a binding domain for the molecule of interest, useful for detecting binding of a molecule of interest.

Claim 8; SEQ ID NO 115; 101pp; English

The present invention describes a recombinant fusion protein (I) for detecting binding of a molecule of interest. (I) comprises: (a) a detecting binding of a molecule of interest. (I) comprises: (a) a detection domain, (b) a first localisation domain, the first localisation domain and the binding domain for the molecule of interest constituting the recombinant fusion protein for detecting binding of a molecule of interest are operably linked. The binding domain for the molecule of interest is separated from the first localisation domain by 0.20 amino acid residues. The first localisation domain by 0.20 amino acid residues. The first localisation domain and the binding compinant for the molecule of interest both do not occur in a single non-recombinant protein with the same spacing as in the recombinant fusion protein; (1) a recombinant expression vector comprising the nucleic acid molecule; (2) a recombinant expression vector comprising the nucleic acid molecule; (3) a squences operably linked to the recombinant mucleic acid molecule; (3) a genetically engineered host cell transfected with the recombinant expression vector; (4) a kit for detecting binding of the molecule of interest, and (5) a method for identifying compounds that alter the binding of the molecule of interest. The recombinant fusion protein is

ö useful for detecting binding of a molecule of interest. The recombinant fusion protein eliminates the need to construct two or more chimeric proteins and enables the monitoring of biochemical events in live, intact or fixed cells. The present sequence is used in the exemplification of the present invention. Gaps ., Query Match 76.0%; Score 19; DB 7; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 3; Conservative 0; Mismatches 0; Indels Assay, binding, target, analyte, enyme activity. Rho 110 labelled leaving group peptide #48. ADC15592 standard; peptide; 4 AA. 21-JAN-2003; 2003WO-US001497. 08-FEB-2002; 2002US-00071395. 18-DEC-2003 (first entry) (BECI) BECKMAN COULTER WO2003067212~A2. 2 PRP 4 Sequence 4 AA; 14-AUG-2003. Synthetic. ADC15592; Bell ML; RESULT 29 ADC15592 ઠે 셤

of of Assaying target analytes in a sample comprises determining the extent binding between the target analyte and the solid support-bound ligand the analyte useful for conducting multiplexed assays of multiple analytes. WPI; 2003-689583/65.

Disclosure; Page 33; 48pp; English.

The invention relates to a method for assaying target analyte(s). The steric interference is provided by a solid support (s1). The method construction interference is provided by a solid support (s1). The method convolution is involves assaying target analyte(s) (A) in a sample comprises providing (A) and binding ligand (1) of (A) bound to a solid support, where the construction is porous, the ligand is bound within the pores of the support of the binding ligand to bind to (A) that does not hinder the binding of all cher target analyte(s) to all other binding ligand so all cher binding ligand to bind to (A) that does not hinder the binding of all cher target analyte (s) simultaneously assaying multiple different analytes and permits each target analyte to be assayed within a dynamic analyte analyte. The method permits assayed to be conducted within their dynamic range without a need to dilute the reactants, therefore, achieving a virtual dilution. The method permits measurement of high concentration analytes in the same reaction mixture as low concentration analytes in the same reaction mixture as low concentration analytes therefore, reducing the number of separate analyses necessary to complete a full clinical menu. The measurement does not require problematic low-affinity receptors and does not significantly expresents a leaving group peptide for use in a cellprobe reagent for represents a leaving group peptide for use in a cellprobe reagent for

2 PRP 4

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The invention relates to a method for assaying target analyte(s). The steric interference is provided by a solid support (s1). The method involves assaying trarget analyte(s) (A) in a sample comprises providing (A) and binding ligand (1) bound to a solid support, where the support is porous, the ligand is bound within the pores of the support ability and the pores sterically interfere with the ability of the chinding ligand to bind to (A) that does not hinder the binding of all other target analyte(s) to all other binding ligand(s). The method is efficiently capable of simultaneously assaying multiple different analytes and permits each target analyte to be assayed within a dynamic assay range for that analyte. The method permits assays to be conducted within their dynamic range without a need to dilute the reactants, therefore, achieving a virtual dilution. The method permits measurement of high concentration analytes in the same reaction mixture as low concentration analytes therefore, reducing the number of separate analyses necessary to complete a full clinical measurement does not require problematic low-affinity receptors and does not significantly affect other analyses in the reaction mixture. The current sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assaying target analytes in a sample comprises determining the extent of binding between the target analyte and the solid support-bound ligand of the analyte useful for conducting multiplexed assays of multiple
                                                                               Gaps
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                                       Length 4;
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                                     76.0%; Score 19; DB 7; Le
Llarity 100.0%; Pred. No. 1.4e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Assay; binding; target; analyte; enyme activity.
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                                                                                                                                                                                                                                                          ADC15585 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                     (first
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                                     Query Match
Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                   2 PRP 4
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Sequence 4 AA;
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                                                                             Matches
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The invention relates to a method for assaying target analyte(s). The steric interference is provided by a solid support (s1). The method involves assaying target analyte(s) (A) in a sample comprises providing (A) and binding ligand (1) of (A) bound to a solid support, where the support is porous, the ligand is bound within the pores of the support ability, and the pores sterically interfere with the ability of the binding ligand to bind to (A) that does not hinder the binding of all other target analyte(s) to all other binding ligand(s). The method is other target analyte(s) to all other binding ligand(s). The method is efficiently capable of simultaneously assaying multiple different analytes and permits each target analyte to be assayed within a dynamic assay range for that analyte. The method permits assays to be conducted within their dynamic range without a need to dilute the reactants, therefore, achieving a virtual dilution. The method permits measurement of high concentration analytes in the same reaction mixture as low analyses necessary to complete a full clinical menu. The measurement does not sequire problement lower in the reaction mixture as significantly affect the require problement of mixture and analyses therefore, reducing the number of separate analyses problement of now and significantly affect there are in the reaction mixture as an analyses problement of mixture and now and significantly affect there are in the reaction mixture and now and significantly affect therefore in the reaction mixture and now and significantly affect therefore in the reaction mixture and now and significantly affect the reaction and now and significantly and remains and now and significantly and the reaction and now and significantly and the same reaction and now and significant of the same reaction and now and significant 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assaying target analytes in a sample comprises determining the extent binding between the target analyte and the solid support-bound ligand the analyte useful for conducting multiplexed assays of multiple
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                                                                                                                                                                                                                                                                                                                                                                          Assay; binding; target; analyte; enyme activity.
                                                                                                                                                                                                                                                                                                                   Rho 110 labelled leaving group peptide #15.
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                                                                                                                                                ADC15559 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-689583/65.
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Best Local Similarity
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PRP 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Matches
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                                                                                                                     ADC15559
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The invention relates to a novel system for reconstitution of osseous tissue comprising a scaffold carrying a compound (1) that promotes bone tissue comprising a scaffold carrying a compound (1) that promotes bone formation and a component that decreases bone resorption (II). (I) induces migration and adhesion of osteoblasts and osteoclasts and (II) inhibits proteolysis (specifically by plasmin) of extracellular matrix.

(I) is preferably selected from: selectin or selectin binding fragments, proteins and peptides that facilitate cell adhesion, plasminogen activator inhibitors, protease inhibitors and metalloprotease inhibitors. The peptides used in the system of the invention. The system is used to replace, remodel or correct bone defects, e.g. fractures, fissures or bone mass loss. Incorporation of (I) into the scaffold results in rapid seeding by osteoblasts and the development of an organic matrix, i.e. the preformed scaffold replaces the rate-determining step of extracellular matrix formation. The scaffold celeigned to have a predetermined resolved; and may include regulatory compounds for
                                                                                                                                                                                                                                                                                                                                                                                             System for reconstructing osseous tissue, useful e.g. for treating fractures, comprises scaffold containing promoter of bone formation and inhibitor of bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Bone regenerative, osteopathic, osseous tissue, reconstitution, scaffold matrix; bone formation promoter, bone resorption inhibitor, cell adhesion, osteoblast, osteoclast, bone defect, fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%; Score 18; DB 3; Length 3; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                            (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Page 31; 44pp; English.
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                                                                                                                                                                                                 99WO-US016800.
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                    WO200004941-A1
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                                                                                                                                                                                                                                       24-JUL-1998;
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Synthetic.
                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                  Budny JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer in
                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                          antiangiogenic; cytostatic; immunosuppressive; antirheumatic;
antiarthritic; anglogenais inhibitor; anglogenesis inhibitor;
autoimmune diseases; rheumatoid arthritis; immune arthritis;
degenerative arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compound useful for inhibiting angiogenesis or treating camamal, or in prevention and treatment of other diseases such autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.0%; Score 19; DB 7; Length 4; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               /label= OTHER
/note= "OTHER= Prolylethylamide"
                                                                                                                                     Angiogenesis inhibiting peptide seq id 12
                                                                                                                                                                                                                                                                                                                                                     /label= OTHER
/note= "OTHER= N-acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 12; 21pp; English.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY80482 standard; peptide; 3 AA.
                    ADD52662 standard; peptide; 4 AA
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                                                                                               (first entry)
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Best Local Similarity 100.
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(BRAD/) BRADLEY M F.
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                                                                                                                                                                                                                                                                                                                  Key
Modified-site
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                                                                                               15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-2003
                                                                                                                                                                                                                                                                            Synthetic
                                                          ADD52662;
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The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a trarget peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptides and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The binding peptide is covalently linked to a 'Cp(aa)Cp' technetium binding group wherin Cp is a protected cysteine and (aa) is an amino acid. The technetium-99m complexes are used to image target sites within a mammalian body. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Technetium-99m labelled polypeptide imaging agent; radiolabeled imaging; radiodiagnostic agent.
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                                                                                           Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%; Score 18; DB 6; Length 3; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of thrombus binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR26394 standard; peptide; 4 AA.
                  Ito T,
                                                                                                                                                                          Claim 8; Page 42; 87pp; Japanese
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(first entry)
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Best Local Similarity 100.
Matches 3; Conservative
                  Nishimura O, Suenaga M,
                                                        WPI; 2003-129302/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9213572-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR26394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR26394
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy! and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a possibilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modiffying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disconders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

Wodifying and attaching therapeutic peptides to allouin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases.

Chabbods to AABD341 represent peptides which can be used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                             Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide production by gene recombination associated peptide #42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand; gene recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                  Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%; Score 18; DB 4; Length 3; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                  Holmes DL,
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 572; 733pp; English.
                                                                                                                                                                                                                  Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU60858 standard; peptide; 3 AA
                                                                                             99US-0134406P.
99US-0153406P.
99US-0159783P.
                                                        17-MAY-2000; 2000WO-US013576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-2002; 2002WO-JP004735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2001; 2001JP-00147341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                  Ezrin AM,
                                                                                                                                                                          (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                       WPI; 2001-112059/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GPR 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3 AA;
                                                                                               17-MAY-1999;
                                                                                                                    10-SEP-1999;
                                                                                                                                       15-OCT-1999;
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                  23-NOV-2000
                                                                                                                                                                                                                  Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU60858;
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Matches
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Synthetic peptides beginning with the sequence Gly-Pro-Arg will bind to fibrinogen and prevent fibrin polymerisation. A scrambling reaction was used to determine whether unique GRP-like peptides could be created from a reaction seeded with GPR and if these new products could bind to fibrinogen. The peptide GPRL was one of the new peptides to be generated by hydrolysis/synthesis of fibrinogen/GPR. It inhibits fibrin polymerisation but its affinity was less than that of GPR or GPRP. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                   Identifying peptide(s) which bond to predetermined targets - by random degradation and recombination of peptide(s) and isolating bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                       platelet aggregation, fibrinogen A-alpha chain, protein scrambling,
GPR-like peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   platelet aggregation, fibrinogen A-alpha chain, protein scrambling,
GPR-like peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%; Score 18; DB 2; Length 4; 100.0%; Pred. No. 1.4e+06; Live 0; Mismatches 0; Indels
                          Fibrinogen binding peptide generated by scrambling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibrinogen binding peptide generated by scrambling.
                                                                                                                                                                                                                                                                                             Le Breton G;
                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 60; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR32385 standard; peptide; 4 AA.
                                                                                                                                                                                                   92WO-US006933
                                                                                                                                                                                                                                91US-00813315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-00813315
01-JUL-1993 (first entry)
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(first entry)
                                                                                                                                                                                                                                                                                          Venton DL, Hopfinger AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                              (RECE-) RECEPTOR LAB INC
                                                                                                                                                                                                                                                                                                                       WPI; 1993-093932/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GPR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4 AA;
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                                                                                                                                                                                                 20-AUG-1992;
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01-JUL-1993
                                                                                                                                      W09304079-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1991;
                                                                                                                                                                  04-MAR-1993.
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                                                                                                                                                                                                                                                                                                                                                                                      peptide(s).
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                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic peptides beginning with the sequence Gly-Pro-Arg (e.g. GPRV) will bind to fibrinogen and prevent fibrin polymerisation. A scrambling reaction was used to determine whether unique GPR-like peptides could be created from a reaction seeded with GPR and if these new products could bind to fibrinogen. See e.g. AAR32379. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying peptide(s) which bond to predetermined targets - by random degradation and recombination of peptide(s) and isolating bound
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                   platelet aggregation, fibrinogen A-alpha chain, protein scrambling, GPR-like peptide.
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                                                                    0; Indels
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                                          Length 4;
                                     72.0%; Score 18; DB 2; Le
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breton G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 58; 89pp; English
                                                                                                                                                                                                           AAR32383 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                    Fibrinogen binding peptide #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92WO-US006933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00813315
                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hopfinger AJ,
                                                                      Conservative
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RECE-) RECEPTOR LAB INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-093932/11.
                                    Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                              1 GPR 3
                                                                                                    1 GPR 3
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         Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               WO9304079-A1.
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                                                                                                                                                                                                                                                                      25-MAR-2003
01-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jenton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                         AAR32383;
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                                                                                                                                                                            RESULT 37
AAR32383
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AAR32384
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WPI; 1994-034983/04.
N-PSDB; AAQ44556.
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUL-1992;
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13-JUL-1994
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                                                         Venton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR48072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stout J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 40
AAR48072
THE STANDARD STANDARD
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In order to produce recombinant polypeptides with C-terminal alpha-amide groups and/or N-terminal acetyl groups, fusion proteins are formed in which the relevant terminus (termini) of the polypeptide is protected by a biological protecting group. The protecting group is a peptide or amino acid having at least one cleavage site for its removal. The sequence AAR48072 represents a suitable biological protecting group, i.e. a Thrombin cleavage site. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A recombinant multicopy fusion protein was formed in which human carbonic anhydrase was connected (via interconnecting peptide AAR46079) to a multicopy polypeptide containing 2 copies of GRF (intraconnected by peptide AAR48079). The inter- and intraconnecting peptide contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal modification, amidation, biological protecting group, N-terminal modification, recombinant multicopy fusion protein; human carbonic amydraes, interconnecting peptide; GRF; intraconnecting peptide, hydroxylamine; chemical cleavage site; thrombin, enzymatic cleavage site; Growth Hormone releasing factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terminal modification of recombinant single copy polypeptide - by protecting, modifying and de-protecting polypeptide, e.g. fusion protein, contg. biologically added protecting gp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intra/Interconnecting peptide containing multiple cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4;
                         Disclosure and Claim 10; Page 22; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
72.0%; Score 18; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 0; Mismatches 0;
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/note= "enzymatic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "chemical cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 80; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR48079 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GPR 3
                                                                                                                                                                                                                                                                                                                                                                     Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR48079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                       Synthetic peptides beginning with the sequence Gly-Pro-Arg will bind to fibrinogen and prevent fibrin polymerisation. A scrambling reaction was used to determine whether unique GPR-like peptides could be created from a reaction seeded with GPR and if these new products could bind to fibrinogen. The peptide GPRF was one of the new peptides to be generated by hydrolysis/synthesis of fibrinogen/GPR. It was less active than GPRL (AAR32384) which was also generated by scrambling; GPRL inhibits fibrin polymerisation but its affinity was less than that of GPR or GPRP. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal alpha-amide polypeptide; amidation; protecting group; N-terminal alpha-acetyl polypeptide; acetylation; recombinant multicopy fusion protein; interconnecting peptide; interconnecting peptide; interconnecting peptide; Blood coagulation; Thrombin; recognition site.
                                                                                                                                                                                                random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                         Identifying peptide(s) which bond to predetermined targets - by degradation and recombination of peptide(s) and isolating bound peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.0%; Score 18; DB 2; Length 4; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biological protecting gp. contg. Thrombin cleavage site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .4
/label= Thrombin_recognition_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmquist
                                                                   Le Breton G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coolidge TR,
                                                                                                                                                                                                                                                                                                                                        Example 5; Page 60; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR48072 standard; peptide; 4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-00912798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                   Hopfinger AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
   (RECE-) RECEPTOR LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BION-) BIONEBRASKA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wagner FW,
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Gaps

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Indels

100.0%; Pred. No. 1.4e+06;

3; Conservative

1 GPR 3

43

Best Local Similarity Matches 3; Conserv

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The inventors claim a method for inexpensively and rapidly producing a large and varied population of peptides and soreening this varied population for the presence of peptides which bind to a target, for example, a macromolecule associated with a particular physiological function. The specific binding peptides are isolated and sequenced, synthesised on a large-scale, their biological activity is demonstrated, and then subjected to clinical testing. The random population of peptides is generated by employing a scrambling system which utlises one or more proceases, esp. papain, pepsin, bromelin, thermolysin, trypsin, promase, chymotrypsin, subtilism and dipppidy peptidase IV. A typical starting proceases, partic. fibringen; sickle cell haemoglobin; collagenase IV; rennin, Gp. IIb IIIa or phospholipase A2. It has been demonstrated that csyptides beginning with the sequence GPR will bind to fibringen. Such peptides include GPR, GFRP and GPRV. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying peptides which binds to a specific target - by contacting target with scrambled equilibrium mixt. of many peptide derived from protein by incubation with protease, for detecting potential therapeutic
                                                                                                                                                                             Gaps
recognition site for a chemical cleavage reagent as well as one for enzymatic cleavage reagent. The multicopy fusion protein is used to produce single copies of GRF modified at the N-terminal with a pyrroglutamyl residue and modified at the C-terminal by amidation. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                               ;
                                                                                                                                                                           0; Indels
                                                                                                                                            Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Random degradation; recombination; scrambling reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of peptide which binds to human fibrinogen.
                                                                                                                                      72.0%; Score 18; DB 2; Le
100.0%; Pred. No. 1.4e+06;
rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 AAR49797 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 54; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93WO-US008231,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-00932200
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(first entrý)
                                                                                                                      Query Match
Best Local Similarity luv...
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hopfinger AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RECE-) RECEPTOR LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-083103/10.
                                                                                                                                                                                                            1 GPR 3
                                                                                                         Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9404558-A1
                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
23-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                    AAR49797;
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                                                                                                                                                                                                                                                                                                              88888888
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Length 4;

DB 2;

72.0%; Score 18;

Query Match

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The inventors claim a method for inexpensively and rapidly producing a large and varied population of peptides and screening this varied population for the presence of peptides which bind to a target, for example, a macromolecule associated with a particular physiological carample, a macromolecule associated with a particular physiological function. The specific binding peptides are isolated and sequenced, synthesised on a large-scale, their biological activity is demonstrated, and then subjected to clinical testing. The random population of peptides is generated by employing a scrambling yetem which utilises one or more proteases, esp. papain, pepsing. The random population of peptides is generated by employing a scrambling yetem which utilises one or more proteases, esp. papain, pepsing peptidase IV. A typical starting protein is casein. Targets are esp. receptors involved in physiological processes, partic. fibrinogen; sickle cell heamoglobin; collagenase IV; cennin; Gp. IID IIIa or phospholipase AZ. It has been demonstrated that synthetic peptides beginning with the sequence GPR will bind to fibrinogen. Such peptides include GPR, GPRP and GPRV. HPLC fractions bound to fibrinogen were screened on CE. Three of these GPR peaks were collected and sequenced and found to be GPRL, GPRF and LPK. In addition, a GPR independent peak was also collected and found to have the sequence EDKPDNF. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying peptides which binds to a specific target - by contacting target with scrambled equilibrium mixt. of many peptide derived from protein by incubation with protease, for detecting potential therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%; Score 18; DB 2; Length 4; 100.0%; Pred. No. 1.4e+06; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                              Random degradation; recombination; scrambling reaction.
                                                                                                                                                                                     Sequence of peptide which binds to human fibrinogen.
                                           AAR49798 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 54; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-00932200.
                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hopfinger AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECE-) RECEPTOR LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-083103/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-1992;
                                                                                                                                                                                                                                                                                                             WO9404558-A1
                                                                                                                        25-MAR-2003
23-AUG-1994
                                                                                                                                                                                                                                                                                                                                                       03-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venton DL,
                                                                                                                                                                                                                                                                        Synthetic.
                                                                                   AAR49798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agents.
RESULT 43
AAR49798
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Blood; fibrin; coagulation; inhibition; thrombin; fibrinogen.

Blood coagulation inhibiting peptide.

07-MAR-1995

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Identifying peptides which binds to a specific target - by contacting target with scrambled equilibrium mixt. of many peptide derived from protein by incubation with protease, for detecting potential therapeutic
                                                                                Random degradation; recombination; scrambling reaction
                                                                peptide which binds to human fibrinogen.
              AAR49799 standard; peptide; 4 AA
                                                                                                                                                                                                                                                           Example, Page 54, 97pp, English.
                                                                                                                                             93WO-US008231.
                                           (revised)
(first entry)
                                                                                                                                                                                        Hopfinger AJ;
                                                                                                                                                                          (RECE-) RECEPTOR LAB INC
                                                                                                                                                                                                     WPI; 1994-083103/10.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4 AA;
                                                                                                                                             09-AUG-1993;
                                           25-MAR-2003
23-AUG-1994
                                                                  Sequence of
                                                                                                                                                                                       Venton DL,
                                                                                                                             03-MAR-1994
                                                                                                Synthetic,
                             AAR49799;
RESULT 44
       AAR4979
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New blood coagulation inhibiting peptide(s) having fibrin-agglutination inhibitory activity - useful for the treatment and prevention of

Claim 1; Page 2; 6pp; Japanese.

thrombosis.

(AGEN) AGENCY OF IND SCI & TECHNOLOGY. (NIHA-) NIPPON HAM KK.

WPI; 1994-245692/30.

93JP-00085678 92JP-00300380

19-MAR-1993;

28-JUN-1994

13-OCT-1992;

JP06179696-A

Synthetic.

The inventors claim a method for inexpensively and rapidly producing a large and varied population of peptides and screening this varied population of peptides which bind to a target, for example, a macromolecule associated with a particular physiological function. The specific binding peptides are isolated and sequenced, synthesised on a large-scale, their biological activity is demonstrated, and then subjected to clinical testing. The random population of peptides is generated by employing a scrambling system which utlises one or more proceases, esp. papain, pepsin, bromelin, thermolysin, trypsin, pronase, chymotrypsin, subtilism and dipeptidyl peptidase IV. A typical starting proceases, partic. fibrinogen, sickle cell haemoglobin, collagenase IV, rennin, Gp. IIb IIIa or phospholipase A2. It has been demonstrated that spiring beginds beginning with the sequence GPR will bind to fibrinogen. Such peptides include GPR, GPRP and GPRV, HPLC fractions bound to fibrinogen were screened on CE. Three of these GPR peaks were collected and sequenced and found too be GPRL, GPRF and LPK. In addition, a GPR-independent peak was also collected and found to have the sequence of CDR PDR. (Updated on 25-MAR-2003 to correct PN field.)

72.0%; Score 18; DB 2; Length 4; llarity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity 1 GPR 3 Matches

AAR60327 standard; peptide; 4 AA.

AAR60327 ID AAR6 XX

RESULT 45

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Gaps

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05-JUL-1995

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The blood coagulation inhibiting peptide conprises L-form amino acids and has fibrin agglutination inhibiting activity. Such peptides (see AAR60327 486035) were synthesisez (applied Blosystems Co., 430A) and purified by high pressure liquid chromatography. To 0.2 ml of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was added and incubated for I minute at 37 deg Celsius. 0.2 ml of thrombin solution was added and the IC50 was determined according to the method of Kawasaki et al. This peptide had an IC50 of 510 micromolar compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombin; inhibitor; aggregation; platelet; determination; assay; qualitative; quantitative; fibrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.0%; Score 18; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.46+06; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW09862 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombin inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GPR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                micromolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW09862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 46
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Synthetic.
                                                             functions
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                                                                                                Query Match
                                                                                                                 Matches
                                                                                                                                                                              RESULT 48
                                                                                                                                                                                         AAR80053
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                                                                                                                                                  In the qualitative or quantitative determn. of thrombin-induced platelet aggregation in the presence of fibrin, interference from fibrin clot formation is suppressed with a fibrin-aggregation inhibitor (e.g. AAM09861-63). The assay may be used to determine the platelet aggregation inhibitory activity of thrombin inhibitors. The peptides inhibit fibrin clot formation at high thrombin concns. without inhibiting platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rich proteins - useful for related to proline rich proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences represented by AAR80046 and AAR80048-R80059 are substrates for the novel peptidase of the invention. The peptidase hydrolyses P-P-P-P, P, P-P-P, and P-P and recognises the proline at the second residue from
                                                                                               Determn, of thrombin-induced platelet aggregation in presence of fibrin comprises use of fibrin aggregation inhibitor to suppress fibrin clot
                                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;
                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                                      1.4e+06;
                                                                                                                                                                                                                                            72.0%; Score 18; DB 2;
100.0%; Pred. No. 1.4e+0:
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AGEN ) AGENCY OF IND SCI & TECHNOLOGY (NIHA-) NIPPON HAM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptidase hydrolyses proline ion and treatment of diseases
                                                                                                                                                                                                                                                                                                                                              AAR80052 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 6; 7pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention and treatment of dis
studies of cerebral functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94JP-00042027
        94EP-00119803
                         93DE-04344919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94JP-00042027
                                                                                                                                   Claim 5; Col 6; 5pp; German.
                                                                                                                                                                                                                                                                                                                                                                                 25-APR-1996 (first entry)
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Best Local Similarity 100.
                                           (BEHW ) BEHRINGWERKE AG
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                                                                              WPI; 1995-233339/31.
                                                                                                                                                                                                                                                                                                                                                                                                    Peptidase substrate
                                                                                                                                                                                                                                                                                                                                                                                                                               cerebral function
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                                                                                                                                                                                                                                                                               1 GPR 3
                                                                                                                                                                                                                            Sequence 4 AA;
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                         30-DEC-1993;
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                                                                                                                                                                                                         aggregation
                                                                                                                 formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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the N-terminal of a peptide to release the N-terminal amino acid. The enzyme's activity is stimulated with Mnol2 and inhibited with ophenanthrollene and 2-mercaptochtanol. The peptidase is useful for the hydrolysis of proline containing physiologically active peptides, oligoproline and proline rich proteins in the living body, particularly oligoproline and proline rich peptidase is useful for the prevention and treatment of proline rich protein related diseases and study of cerebral
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Pred. No. 1.4e+06;
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Modified-site
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Pollak A,
                               imaging.
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                                                                                                                                                                                                                                                                                                                                                                                                      Transpeptidation of recombinant polypeptides - using endopeptidase such as trypsin or thrombin to modify C-terminal residue.
                     Gaps
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                                                                                                                                                                                     Interconnecting peptide for the fusion protein construct GRF 1-41.
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 Score 18; DB 2; Length 4;
Pred. No. 1.4e+06;
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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                                                                                                               AAR69071 standard; peptide; 4 AA.
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 72.0%;
75.0%;
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                     3; Conservative
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Query Match
Best Local Similarity
Matches 3; Conserv
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26-OCT-1995
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AAW11088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide derived radionuclide chelators and metal complexes - useful diagnostic imaging.
Leukocyte; target; direct; chelator; radionuclide; radiolabel; isotope; atherosclerosis; thrombosis; embolism; infection; thrombus; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00279155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RESO-) RESOLUTION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodbody A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Wed Sep 8 05:50:41 2004
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7	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2											RESULT 1 US-07-934-553-5 Sequence 5, Appl Patent No. 5314Pl Patent			
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	Run on: September 7, 2004, 18:54:02; Search time 31 Seconds (without alignments) 6.661 Million cell updates/sec	Title: US-09-931-009A-2 Perfect score: 25 Sequence: 1 GPRP 4	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 389414 segs, 51625971 residues	Total number of hits satisfying chosen parameters: 389414	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65 summaries	Database : Issued_Patents_AA:* 1: /egn2_6/ptodata/2/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:* 3: /egn2_6/ptodata/2/iaa/6A_COMB.pep:* 4: /egn2_6/ptodata/2/iaa/6B_COMB.pep:* 5: /egn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /egn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	25 100.0 4 1 US-07-934-553-5 25 100.0 4 1 US-07-934-553-5 25 100.0 4 1 US-08-022-381A-1 25 100.0 4 1 US-08-225-474-5 25 100.0 4 1 US-08-35-759-2 25 100.0 4 2 US-08-475-827A-1 25 100.0 4 2 US-08-75-827A-1 25 100.0 4 2 US-08-75-749-6 25 100.0 4 2 US-08-75-3-781-2 25 100.0 4 2 US-08-75-3-781-2 25 100.0 4 4 US-09-241-65-6 25 100.0 4 4 US-09-241-6-6 25 100.0 4 4 US-09-241-6-6 25 100.0 4 4 US-09-241-6-6 25 100.0 6 4 US-09-241-6-6 25 100.0 6 4 US-09-241-6-6 25 100.0 6 7 US-08-02-381A-5 25 100.0 5 1 US-08-022-381A-6 25 100.0 5 1 US-08-022-381A-7 25 100.0 5 1 US-08-022-381A-7 25 100.0 5 1 US-08-022-381A-1		

equence 13, equence 14, equence 2, equence 3, equence 3, equence 4,	equence 5, equence 6, equence 8, equence 9, equence 11, equence 12, equence 12,	equence 15, equence 15, equence 1, equence 16, equence 17, equence 18, equence 20,	Sequence 16, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 20, Appl Sequence 21, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 105, Appl Seq
08-022-381A-08-022-381A-08-022-381A-08-475-827A-08-475-827A-08-475-827A-08-475-827A-08-475-827A-	08-475-827A 08-475-827A 08-475-827A 08-475-827A 08-475-827A 08-475-827A 08-475-827A	08-475-8774-1 08-475-8774-1 08-672-255-1 08-022-38174-1 08-022-38174-1 08-022-38174-1 08-022-38174-1 08-022-38174-1 08-022-38174-1	08-475-8274-08-475-8274-08-475-8274-08-475-8274-08-475-8274-08-475-8274-08-475-08-484-773-08-484-773-09-721-970-
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ALIGNMENTS

Sequence 5. Application US/07934553

Patent No. 5314690

Patent No. 5314690

GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALLON, LUNGANUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILINOIS
COUNTY: USA
ZIP: GOOGO-4002
COUNTY: USA
ZIP: GOOGO-4002
COUNTY: USA
ZIP: GOOGO-4002
COUNTY: USA
ZIP: GOOGO-4002
COUNTY: USA
ZIP: BADABLE FORM:
MEDIUM TYPE: PLODS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,553
FILING DATE: 19920821
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/934,553
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:

```
APPLICANT: Stuber, Werner
APPLICANT: Stickenscher, Karl
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
CORRESPONDENCE: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
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APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: 1gF Mediated Allergies
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: 1. 1300 1 SCIENC, N.W., SULCE / 00
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPOTER: PELLIN DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 06-MAY-1991
RAPPLICATION NUMBER: D6-MAY-1991
RAPPLICATION NUMBER: DE 40 14 655.3
FILING DATE: -08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: MARKAWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REGERANCE/DOCKET NUMBER: 36,351
REBERNOR-JOCKET NUMBER: 36,351
RELEBROOMENTION INFORMATION:
TELEBROOME: 202-406-4000
                                                                                                                     Sequence 1, Application US/08022381A
Patent No. 5478810
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Patent No. 5560915
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTON, DUANE L.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: HOPFINGER, ANTON J.
APPLICANT: LE BRETON, GENERATING AND SCREENING
TITLE OF INVENTION: WEBFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: WASHINGTON
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 1; Length 4;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 25; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppd disk
MEDIUM TYPE: Floppd disk
MEDIUM TYPE: Floppd disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/932,200
FLING DATE: 21-AUG-1992
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
RESTENCE/DOCKET NUMBER: VENTON=1B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/07932200
Patent No. 5366862
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-934-553-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C.
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GPRP 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-932-200-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-932-200-6
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Gaps

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Tilton, Fallon, Lungmus & Chestnut

ADDRESSEE:

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Patent No. 5607859
Sequence 1, Application US/08475827A
Patent No. 5607859
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Preparation Thornol Inhibitors
NUMBER OF SEQUENCES: 22
CORRESSONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Punner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                    .
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100.0%; Score 25; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPREY: USA

ZIP: D.C.

COMPUTER: D.C.

COMPUTER: D.C.

COMPUTER: PACABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,827A

FILING DATE: 07-JUN-1995

CLASSIPPLICATION: 436

PRICK APPLICATION DATA:

APPLICATION NUMBER: US 08/022,381

FILING DATE: 06-MAY-1991

PRILING DATE: 06-MAY-1991

PRILING DATE: 06-MAY-1991

PRILING DATE: 06-MAY-1991

PRILING DATE: 08-MAY-1990

APPLICATION NUMBER: DE 40 14 655.3

FILING DATE: 08-MAY-1990

APPLICATION NUMBER: DE 40 14 655.3

FILING DATE: US 08-MAY-1990

APPLICATION NUMBER: DE 40 14 655.3

FILING DATE: US 08-MAY-1990

APPLICATION NUMBER: DE 40 14 655.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Johnson, Lori-Ann
REGISTRATION NUMBER: 34,498
REFRENCE/DOCKET NUMBER: 05552
TELECOMMUNICATION INPORMATION:
TELEPAK: (202) 408-4400
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
             REFERENCE DOCKET NUMBER: 0555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION FOR END INO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 mmino acids
  35,391
                                                                                                                                                                                           ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-365-759-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-08-475-827A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: U.S.A.
ZIPE: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TROPP COMPATIBLE
COMPUTER: DATE: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,759
FILING DATE: 20-DEC-1994
' ASSIFICATION: ....TOPEC-1994
                                                                                                                                                                                                         OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-AAY-1991
ATTORNEY/AGENT INFORMATION:
NAMME: Tilton, Timothy L.
REGISTRATION NUMBER: US 07/705,071
FILING DATE: 24-AAY-1991
ATTORNEY/AGENT INFORMATION:
NEGISTRATION NUMBER: MU 9033-CIP2
TELEPHONE: (312)-456-8000
TELEPHONE: (312)-456-8776
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCOMMITION:
APPLICANT: Reers, Martin
TITLE OF INVENTION: Method for Determining Platelet
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
100 S. Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-365-759-2; Sequence 2, Application US/08365759; Patent No. 5563041
                                                                                           ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-225-474-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                     Chicago
Illinois
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                                                                        COUNTRY: USA
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Gaps
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Indels
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Mismatches
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4; Conservative
Matches
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; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
US-09-540-448-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Sequence 6, Application US/09540448

GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TILLE OF INVENTION: Charged Lipids and Uses For The Same FILE REFERENCE: UNGR1592

CURRENT PILLICATION NUMBER: US/09/540,448

CURRENT FILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 3; Length 4; 100.0%; Pred. No. 3e+05; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 4; Length 4; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,395
FILING DATE: 06-Mar-1996
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-048
TELLECHANTONICATION INFORMATION:
TELLEPHONE: (617) 248-7000
TELLEFAX: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; ; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-08-611-395-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/09243640
; Patent No. 6521211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                        ZIP: 02110
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.v
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Best Local Similarity 100.
Matches 4; Conservative
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US-08-993-165-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6129923
GENERAL INFORMATION:
RAPLICANT: Unger, Yann C
APPLICANT: Unger, Yann C
APPLICANT: Wo, Yungiu
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
FILE REPRENCE: UNGRI224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
APPLICANT: Swenson_______Stephen
APPLICANT: Swenson_______Stephen
APPLICANT: Flores Sanchez, Eladio
TITLE OF INVENTION: THROMBOLYTIC ACENTS WITH ANTITHROMBOTIC ACTIVITY
FILE REFERENCE: DITI 1200
CURRENT APPLICATION NUMBER: US/08/753,781C
CURRENT FILING DATE: 1996-12-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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OTHER INFORMATION: Description of Artificial Sequence:synthetic
OTHER INFORMATION: peptide
US-08-753-781-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 25; DB 3; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 2; Length 4; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08611395

Patent No. 6166939

GENERAL INFORMATION:

APPLICANT: SASAKI, MASAHIRO

BOSMAN, BOUKJE

TAN, PARIS S. T.

TAKFUOT, SHIN'ICHI
INASAKI, TAISUKE

INASAKI, TAISUKE

INASAKI, TAISUKE

OORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

STREET: 125 High St.

CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPRP 4
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US-08-611-395-5
                                                                                                                                                                                                                  LENGTH:
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                           TITLE OF INVENTION: WETHOD FOR GENERATING AND SCREENING
TITLE OF INVENTION: USEFUL PEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIWARK
STREET: 419 SEVENTH STREET, N.W.
CITY: WASHINGTON
STREET: U.S.A.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTENTION NUMBER: PCT/US93/06231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC TITLE OF INVENTION: DOMAINS OF TRANSMEMBRANE RECEPTORS NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: PCPPY disk COMPUTER: PC COMPATIBLE OPERATING SYSTEM: PC COMPATIBLE OPERATING SYSTEM: PC COMPATIBLE OPERATING SYSTEM: PC COMPATIBLE OPERATING SYSTEM: PC COMPATIBLE OPERATION NUMBER: PCT/US95/07542
FILING DATE: 13-UTM-1995
FILING DATE: 13-UTM-1995
FILING DATE: 13-UTM-1994
INFORMATION FOR SEG ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9507542
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICALLO.
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 26,005
REFERENCE/DOCKET NUMBER: VENTC
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-737-3528
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
         LE BRETON, GUY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
GY: linear
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PCT-US95-07542-4
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               GENERAL INFUGNATION:
GENERAL INFUGNATION:
APPLICANT: Winger, Evan C
APPLICANT: Winger, Evan C
APPLICANT: Winger, Dekarg
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
FILE REFERENCE: DUP-0463
CURRENT APPLICATION NUMBER: US/09/243,640
CURRENT FILING DATE: 1996-02-03
PRIOR APPLICATION NUMBER: 08/660,032
PRIOR APPLICATION NUMBER: 08/640,464
PRIOR APPLICATION NUMBER: 08/640,464
PRIOR APPLICATION NUMBER: 08/497,684
PRIOR FILING DATE: 1996-05-01
PRIOR PLING DATE: 1998-02-02
PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/073,913
PRIOR APPLICATION NUMBER: 60/073,913
PRIOR APPLICATION NUMBER: 60/073,913
PRIOR APPLICATION NUMBER: 20/073,913
PRIOR APPLICATION NUMBER: 20/073,913
PRIOR APPLICATION NUMBER: 60/073,913
PRIOR APPLICATION NUMBER: 80/073,913
PRIOR APPLICATION NUMBER: 80/073,913
PRIOR APPLICATION NUMBER: 20/073,913
PRIOR APPLICATION NUMBER: 80/073,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08929847

Patent No. 6548047

Batent No. 6548040

GENERAL INFORMATION:
APPLICANT: Under, Evan C.
TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
FILE REFREENCE: BMS0441

CURRENT APPLICATION NUMBER: US/08/929,847

CURRENT FILING DATE: 1997-09-15

NUMBER OF SEQ ID NOS: 39

SEQ ID NO 6

LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence
JS-09-243-640-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n 100.0%; Score 25; DB 4; Length 4; Similarity 100.0%; Pred. No. 38+05; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Completely synthetic sequence US-08-929-847-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
PCT-US99-08231-6
SGQUENCE 6, Application PC/TUS9308231
; GENERAL INFORMATION:
APPLICANT: VENTON, DUANE L.
; APPLICANT: HOPFINGER, ANTON J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GPRP 4
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US-08-929-847-6
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PARENT NO. 5474810

APPLICANT: Etuber, Werner

APPLICANT: Etuber, Werner

TITLE OF INVENTION: Peptide Anides, Processes for the

TITLE OF INVENTION: Peptide Anides, Processes for the

TITLE OF INVENTION: Peptide Anides, Processes for the

TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett & ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington Street, N.W., Suite 700

CONTRY: Nashington Compatible

COMPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER TEAD COMPATA: Po-DoS/MS-DOS

SOFTWARE: Ploppy disk

COMPUTER TEAD STREET: 993 (2022,381A

TILING DATE: 04-MAY-1991

PRIOR APPLICATION NUMBER: US 07/696,085

FILING DATE: 06-MAY-1991

PRIOR APPLICATION NUMBER: US 07/696,085

TILING DATE: 06-MAY-1991

PRIOR APPLICATION NUMBER: US 07/696,085

TILING DATE: 08-MAY-1990

TELECOMOUNICATION NUMBER: 05-08-400

TELECOMOUNICATION
Sequence 3, Application US/08022381A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-08-022-381A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 19
US-08-022-381A-4
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Sequence 2, Application US/08022381A;
Sequence 2, Application US/08022381A;
Patent No. 547810N;
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
CITY: Washington
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                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                100.0%; Score 25; DB 5; Length 4; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 2006-3315
COUNTRY: USA
ZIP: 2006-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/02,381A
FILING DATE: 24 FEB-1993
CLASSIFICATION A514
PRICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRICA APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAMMER: NAMMER: READBLE APPLICATION NUMBER: US WAY-1990
ATTORNEY/AGENT INFORMATION:
NAMMER: NAMER: NAMER: NAMER: NAMMER: NAMER: N
                                                  Ligand sequence recognized by integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REPERENCE, DOCKET NUMBER: 05552.1054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202-408-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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PCT-US95-07542-4
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Sequence 4, Application US/08022381A

Patent No. 5478810

GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Perpide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunner
                                                            ;
                100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 1300 I Street, N.W., Suite 700 Washington
Query Match
Best Local Similarity luv...
34 Conservative
                                                                                                           1 GPRP
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linear

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ORIGINAL SOURCE:

100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100... 4, Conservative

1 GPRP 4

RESULT 18 US-08-022-381A-3

us-09-931-009a-2.open.rai

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Length 5;
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APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION T514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1;
100.0%; Pred. No. 3e+05;
iive 0; Mismatches 0
                                                                                                 REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 0552.1054-01000
TELECOMMUNICATION INFORMATION:
TELEFANCE: 202-408-4400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05552.1054-01000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08022381A
Patent No. 5478810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REPRENCE/DOCKET NUMBER: 0555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-400
TELEFAX: 202-408-4400
                                     FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Markowicz, Karen R.
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 4, Conservative
                                                                                                                                                                                                                                                                               5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                TYPE: amino acid

TOPOLOGY: linear

// MOLECULE TYPE: peptide

US-08-022-381A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING APPLICATION TO BATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: US/056,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: US/055.3
FILING DATE: 08-MAY-1990
ATTONEY/AGENT INFORMATION:
NAME: MARKANIZZ, KATEN R.
REGISTRATION NUMBER: 05.351
REGISTRATION NUMBER: 05.22.1054-01000
TELEPHONE: 202-408-4000
TELEPHONE: 202-408-4000
INFORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TUMMET: FAMILY SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTE: USAS
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEATON: PC-DCS/MS-DCS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08022381A Patent No. 5478810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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GENERAL INFORMATION:

APPLICANT: Stuber, Werner

APPLICANT: Stuber, Karl

APPLICANT: Elekenscher, Karl

TITLE OF INVENTION: Petride Amides, Processes for the

TITLE OF INVENTION: Preparation Thereof and Agents Containing These as

TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner
;
0
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; 0

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APPLICANT: Stuber, Werner
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
STATE: DC
STATE: DC
                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 2006-3315

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: US-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING ADTE: 06-MAY-1991
PRIOR APPLICATION NUMBER: DE 40 14 655.3
FILING ADTE: OB-MAY-1991
RICHARTONEY/AGENT INFORMATION:
NAME: MARKOWICZ, KATEN R.
REGISTRATION NUMBER: 36,351
REJERRATION NUMBER: 36,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                Sequence 7, April cation US/08022381A
Patent No. 5478810
GENEAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Prizin/Thrombin Clotting Inhibitors
NUMBER OF SEGUENCES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                    Gaps
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100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                               Score 25; DB 1; Length 5; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-022-381A-8
; Sequence 8, Application US/08022381A
; Patent No. 5478810
                                               100.0%;
                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
US-08-022-381A-6
                                                                                                                                                                                                                                                                        RESULT 22
US-08-022-381A-7
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GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Karl
APPLICANT: Fickensoher, Karl
TITLE OF INVENTION: Preparation Thereof and Agents Containing These
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                         Gaps
                                                                                                                                         .;
0
                                                                                               ; Score 25; DB 1; Length 5;
; Pred. No. 3e+05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  US-08-022-381A-9; Sequence 9, Application US/08022381A; Patent No. 5478810
                                                                                               100.0%;
100.0%;
                                                                                                                                       Conservative
                                    MOLECULE TYPE: peptide
                                                                            amino acid
                     linear
TYPE: ami
TOPOLOGY:
                                                         US-08-022-381A-8
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0

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GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner ADDRESSEE: 1300 I Street, N.W., Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIREBI: 1300 I SULEEU, N.M., SULEE / O. STATE: 0.00 COUNTRY: USA

COUNTRY: USA

CONFUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk

COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CLASSIFICATION DATA: Release #1.0, Version #1.25

CLASSIFICATION NUMBER: US/08/022,381A

FILING DATE: 24-FEB-1993

CLASSIFICATION NUMBER: US 07/696,085

FILING DATE: 06-MAY-1991

PRIOR APPLICATION NUMBER: US 07/696,085

FILING DATE: 08-MAY-1991

PRIOR APPLICATION NUMBER: DE 40 14 655.3

FILING DATE: 08-MAY-1990

ATTORNEY/AGENT INFORMATION:
NAME: MARKWAICZ, KARPEN R.

REGISTRATION NUMBER: 36,385.7

REGISTRATION NUMBER: 36,385.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,351
ER: 05552.1054-01000
                                                                                                          05552,1054-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-022-381A-11
; Sequence 11, Application US/08022381A
; Patent No. 5478810
                                       NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351,
REFERENCE/DOCKET NUMBER: 0555,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity luv.
4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-022-381A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TILLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Cont.
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Princegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SUSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 24-FEB-1993
CLASSIFICATION NUMBER: US 07/696,085
PRIOR APPLICATION NUMBER: US 07/696,085
PRIOR APPLICATION NUMBER: DE 40 14 655.3
PRIOR APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: MARKONICATION NUMBER: 05552.1054-01000
TELEPRATION NUMBER: 05552.1054-01000
TELEPRATION NUMBER: 05552.1054-01000
TELEPRAX: 202-408-4400
INFORMATION PRORMATION:
TELEPRAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION 314
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATE: DE 40 14 655.3
FILING DATE: 08-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08022381A
Patent No. 5478810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-022-381A-10
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RESULT 29
US-08-022-381A-14

US-08-022-381A-14

Sequence 14, Application US/08022381A

Sequence 14, Application US/08022381A

Sequence 14, Application US/08022381A

Sequence 14, Application US/08022381A

SEQUENCES: Studence, Warner

APPLICANT: Fickenscher, Karl

TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors

TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors

MUMBER OF SEQUENCES:

ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington
                                TITLE OF INVENTION: Peptide Amides, Processes for the TITLE OF INVENTION: Preparation Thereof and Agents Containing These as TITLE OF INVENTION: Preparation Thereof and Agents Containing These as TITLE OF INVENTION: 22
CORRESPONDENCES: 22
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Mashington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.

ZIP: 20005-3345

COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURBYT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION NUMBER: US/08/022,381A
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: DE 40
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: MATKOWICZ, KATEN R.
FREERENCE, 202-408-4400
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
LEBROTHE S amino acids
TTELEONE: Amino acids
TUBNOTH: S amino acids
TUBNOTH: Amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08022381A; Sequence 12, Application US/08022381A; Sequence 12, Application US/08022381A; Patcent No. 5478810; Patcent No. 5478810; Patch No. 5478810; Patch No. 5478810; Patch No. 547881; TILLE OF INVENTION: Peptide Amides, Processes for the TITLE OF INVENTION: Preparation Thereof and Agents Containing These as TITLE OF INVENTION: Prizin/Thrombin Clotting Inhibitors; NUMBER OF SEQUENCES: 22 CORRESPONDECE ADDRESSE: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700; CITY: Washington Containing These as ADDRESSEE: Punner STREET: Dunner STREET: Dunn
                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                Gaps
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    100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05;
                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTRY: USA

CONTRY: USA

CONTRY: USA

CONTRY: CONTRY: CONTRY

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-COMPATIBLE

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/022,381A

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/696,085

FILING DATE: 06-MAY-1991

PRIOR APPLICATION NUMBER: DE 40 14 655.3

PTILING DATE: 08-MAY-1991

PRIOR APPLICATION NUMBER: B 40 14 655.3

ATTORNEY/AGENT INFORMATION:

NAME: MARKWAICZ, KAREN R.

REGISTRATION NUMBER: 36,351

REFERENCE/COCKET NUMBER: 36,351

REFERENCE/COCKET NUMBER: 05552.1054-01000

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-08-022-381A-13
Sequence 13, Application US/08022381A
Patent No. 2478810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Sequence 2, Application US/08475827A
Patent No. 5607858
GENERAL INFORMATION: Wenner
APPLICANT: Stuber, Wenner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These AS
TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS: ADDRESS: ADDRESSEE: Dunner ADDRESSEE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COUNTRY: USA
ZIP: 10.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER: ERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
                                               05552.1054-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/022,381
FILING DATE: 24-FEB-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRICK APPLICATION NUMBER: US 07/696,085
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION: (202) 408-4000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amin
                                    REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34,498
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REGISTRATION NUMBER: 34, 496
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION: INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                       5 amino acids
                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                   US-08-022-381A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 31
US-08-475-827A-2
                                                                                                                                                                                                                                                    LENGTH:
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Patent No. 5478810
GENERAL INFORMATION: Werner
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andreson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: USONG-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PREDEDICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FILING DATE: 24-FEB-1993
CLASSIFICATION NUMBER: US/096,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
PILING DATE: 24 FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 1;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFERENCE POCKET NUMBER: 0552.1054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB Similarity 100.0%; Pred. No. 3e+4; Conservative 0; Mismatches
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                                                                                                                                                                PILING DATE: 24-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATE: US 07/696,085
FILING DATE: 06-MAY-1991
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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US-08-022-381A-15
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RESULT 33
US-08-475-87A-4
is Sequence Application US/08475827A
is Sequence Application US/08475827A
is General No. 5607658
is GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Florin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
STATE: D.C.
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08475827A
Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
CUUNTEX: USA
ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUW TYER: CIPPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING APPLICATION NUMBER: US/08/475,827A
FILING APPLICATION NUMBER: US/08/475,827A
FILING DATE: 24-FEB-1993
PRICK APPLICATION NUMBER: US/096,085
FILING DATE: G-MAY-1991
PRICK APPLICATION NUMBER: DE 40 14 655.3
FILING APPLICATION NUMBER: DE 40 14 655.3
FILING APPLICATION NUMBER: DE AMAY-1990
ATTONINY/AGENT INFORMATION:
NUMBER: US AMAY-1990
ATTONINY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Johnson, Lori-Ann
REGISTRATION NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 0552.1054-02000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
US-08-475-827A-5
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                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08475827A

Batent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These AS
TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES:
CORRESPONDINCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                            Gaps
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                                                    Query Match 100.0%; Score 25; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,027A

FILING DATE: US/08/475,027A

FILING DATE: US/08/475,027A

PRICK APPLICATION NUMBER: US/08/475,027A

PRICK APPLICATION NUMBER: US/08/022,381

FILING DATE: 24-FEB-1993

PRICK APPLICATION NUMBER: US 07/696,085

FILING DATE: 06-MAY-1991

PRICK APPLICATION NUMBER: US 07/696,085

FILING DATE: 06-MAY-1990

ATORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 34,498

REGISTRATION NUMBER: 34,498

REGISTRATION NUMBER: 34,498

REGISTRATION NUMBER: 34,498

REGISTRATION NUMBER: 05552.1054-0200

TELEPHONE: (202) 408-4000

TELEPHONE: (202) 408-4000

INFORMATION FOR SEQ ID NO: 3:

SEQUIRORE CHARACITERIZE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700 STREET: D.C. STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                      1 GPRP 4
                                                                                                                                                                                                                                                                                                       US-08-475-827A-3
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       US-08-475-827A-2
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Gaps

8 g

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FILING DATE: 07-JUN-1995
CLIASSIFICATION: 436
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/022,381
FILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08475827A Patent No. 5607858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GPRP 4
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Patent No. 5607858
GENERAL INFORMATION.
RAPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunner
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                               ALDKESSEE: Dunner
ALDKESSEE: Dunner
STREEF: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUW TYEB: FILOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING APPLICATION HATA:
APPLICATION NUMBER: US/08/022,381
FILING BAPELCATION NUMBER: US/08/022,381
FILING APPLICATION NUMBER: DS PLICE APPLICATION DATA:
APPLICATION NUMBER: DS PLICE APPLICATION:
ATTANEN APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DS PLICE APPLICATION:
ATTANEN APPLICATION:
AND ATTANEN APPLICATION APPLICATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Unmer STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Johnson, Lori-Ann
REGISTRATION NUMBER: 34,498
REPERENCE'DOCKET NUMBER: 05552,1054-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20005-1315 COMPUTER REDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
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STRANDEDNESS: si
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Best Local Similarity
Matches 4; Conserv
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GENERAL INFORMATION:

APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:

ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OSPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN ROLOS/MS-DOS
SOFTWARE: PATENTIN ROLOS/MS-DOS
TILING DATE: 07-JUM-1995
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: 07-010-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,381
FILING DATE: US 08/022,381
FILING DATE: US 08/022,381
FILING DATE: US 07/696,085
FILING DATE: US 07/696,085
FILING DATE: US 07/696,085
FILING DATE: US 08-MAY-1991
PRIOR APPLICATION NUMBER: US 07/696,085
FILING DATE: US 08-MAY-1991
FILING DATE: US 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSON, LOTI-Ann
REGISTRATION NUMBER: 34,498
FILING DATE: US 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSON, LOTI-AND
REGISTRATION NUMBER: 34,498
FILERPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: S amino acid
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us-09-931-009a-2.open.rai

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CENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Karl
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Finnegan, Henderson, Farabow, Garrett & E: Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,498
ER: 05552.1054-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION 1913.

APPLICATION 10ATA.
APPLICATION DATA.
FILING DATE. 24 FEB-1993
FILING DATE. 24 FEB-1993
PRIOR APPLICATION DATA.
APPLICATION DATA.
APPLICATION DATA.
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
APPLICATION NUMBER: DE 71 FILING DATE: 08-MAY-1990
ATTORNEY AGENT NEORMATION:
NAME: JOHNSON, LOCIT-AND
REGISTRATION NUMBER: 34,498
REFERRINCE/DOCKET NUMBER: 0552.1054-0
TELECHONE: (202) 408-4400
TELECHONE: (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08475827A Patent No. 5607858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 amino acids
                                                                                             TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-827A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 4; Conserv
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ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-475-827A-9
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                                                                                                                                                                                                                                                                                                                                                                    Matches
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Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Warner
APPLICANT: Pickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES:
CORRESPENDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: WESTINGTON

COUNTRY: USA

ZIF: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATER: PACHOLIS
CASSIFICATION NUMBER: US/08/475,827A
FILING DATE: 24-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,381
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: US 07/696,085
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NUMBER: US-MAY-1990
ATTORNEY/AGENT INFORMATION:
NUMMER: LOBER ADDISONATION
NUMBER: L
FILING DATE: 06-MAY-1991

PRICR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY AGENT INFORMATION:
NAME: JOHNSON, LOZI-Ann
REGISTRATION NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 05552.1054-02000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELECOMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05552.1054-02000
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REGISTRATION NUMBER: 34,498
REPERENCE/DOCKET NUMBER: 055
TELECOMMINICATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202) 408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPRP 4
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US-08-475-827A-8
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APPLICANT: Stuber, Werner
APPLICANT: Stokenscher, Karl
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
CORRESPONDENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-68-475-827A-12
Sequence 12, Application US/08475827A
Sequence 12, Application US/08475827A
Sequence 12, Application
Sequence 12, Application
Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700. CITY: Mashington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: 0.7-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05552.1054-02000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 0'-JUN 1995
CLASSIFICATION: 436
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/022,381
FILING DATE: 24-FEB-1993
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRICA APPLICATION DATA: APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1990
ATTONNEY/AGENT INFORMATION:
NAME: JOHNSON, LOXI-AAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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REGISTRATION NUMBER: 34,98
REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 408-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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GENERAL INFORMATION:
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STREET: 1
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 41
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                                                                                                                                                                                                                                     US-08-475-827A-10
Sequence 10, Application US/08475827A
Sequence 10, Application US/08475827A
Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Warl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PELLING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381
FILING DATE: 24-FEB-1993
PRIOR APPLICATION NUMBER: US 08/022,381
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: DE 40 14 655.3
FILING APPLICATION NUMBER: DE ADATA:
ADATA: DE ADATA:
ADATA: DE ADATA: DE ADATA:
ADATA: DE ADATA: DE ADATA: DE 
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Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Johnson, Lori-Ann
REGISTRATION NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 05552.1054-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDRESSEE: Finnegan, Henderson, Farabov ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: USA
ZIP: 20006-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 11, Application US/08475827A; Patent No. 5607858
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4; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                        1 GPRP 4
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US-08-475-827A-11
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Matches
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Gaps

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GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Merner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Pibrin/Thrombin Clotting Inhibitors
NUMBER OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
CORRESPONDENCE: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                             05552.1054-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, N.W., Suite 700 CITY: Washington STATE: D.C. COUNTY: USA ZIP: 20005-3315 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk.
PILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PILING DATE: 24-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: B£ 40 14 655.3
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 40 14 655.3
FILING DATE: 08-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: JOHNSON, LOTI-AMN
RGGISTRATION NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 34,498
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION: 07-JUN-1995
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/022,381
FILING DATE: 24-FBB-1993
PRIOR APPLICATION DATA:: US 07/696,085
APPLICATION NUMBER: US 07/696,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: DE 40 14 655.3
08-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-475-827A-14
; Sequence 14, Application US/08475827A
; Patent No. 5607858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 5 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-MAY-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
FILING DATE: 08-MAY-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-475-827A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08475827A
Sequence 13, Application US/08475827A
Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Studer, Werner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
TITLE OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
COUNTY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: US/08/475,827A
FILING DATE: US/08/475,827A
FILING DATE: US/08/475,827A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381
FILING DATE: 24-FEB-1993
PROR APPLICATION NUMBER: US 08/022,381
FILING DATE: 24-FEB-1993
PRIOR APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1990
ATFORNEY/AGENT INFORMATION:
NAME: Uchason, Lori-Ann
REGISTRATION NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 34,498
RELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4000
TELEFAX: (202) 408-4000
TELEFAX: (202) 408-4000
TELEFAX: (202) 408-4100
TELEFAX: (202) 408-4100
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                   CITY:
STATE:
D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"MEDIUM TYPE: Floppy disk
"MEDIUM TYPE: Ploppy disk
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                 Washington
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US-08-475-827A-13
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Sequence 4, Application US/08595718A Patent No. 5723579
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SEQUENCE CHARACTERISTICS:
LENGTH: 5
                                                                                                                                                                                                                                                                       4; Conservative
                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-475-827A-15
                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           1 GPRP 4
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Patent No. 5607858
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Stuber, Warner
APPLICANT: Fickenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes For the
TITLE OF INVENTION: Preparation Thereof And Agents Containing These As
TITLE OF INVENTION: Fibrin/Thrombin Clotting Inhibitors
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUMPRY: USA

ZIP: 2005-3315

COMPUTER READBLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN RC-BOS/MS-DOS
SOFFWARE: PATENTIN RD-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,827A
FILING DATE: O7-UM-1995
CLASSIFICATION: 436
PRIOR APPLICATION THORER: US 08/022,381
FILING DATE: 24-FEB-1993
PRIOR APPLICATION NUMBER: US 08/022,381
PRIOR APPLICATION NUMBER: DG-MAY-1991
PRIOR APPLICATION NUMBER: DG-MAY-1991
APPLICATION NUMBER: DG-MAY-1991
APPLICATION NUMBER: DG-MAY-1991
APPLICATION NUMBER: DG-MAY-1991
APPLICATION NUMBER: DG-MAY-1990
ATTOREX/AGENT INFORMATION:
MAND: ADALOG ATTORED AND ATTORED AND ATTORED AND ATTORED ATTORED AND ATTORED AND ATTORED AND ATTORED ATTOR
                               NAME: Johnson, Lori-Ann
REGISTRAINON NUMBER: 34,498
REFERENCE/DOCKET NUMBER: 0552,1054-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34,498
ER: 05552.1054-02000
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REGISTRATION UNDRER: 34,98
REFRENCE/DOCKET NUMBER: 0555
TELEPHONE: (202) 408-400
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Lori-Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                           5 amino acids
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
HOLECULE TYPE: peptide
US-08-475-827A-14
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Gaps
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STRANDEDNESS: single strand
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
PUBLICATION INFORMATION:
AUTHORS: Kuyas, C.
AUTHORS: Walder, P.
AUTHORS: Straub, P. W.
TITLE: Isolation of Human Fibrinogen and its
TITLE: Arg-Pro-Lys-Practogel
JOGNAAL: Thromb. Haemost.
VOLUME: 63
ISSUE: 189-444
DATE: 28-JUN-1990
                                                                                                ö
100.0%; Score 25; DB 1; Length 5; 100.0%; Pred. No. 3e+05;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPESSED BAYER OF SEQUENCES:
ADDRESSE: BAYER CORPORATION
STREET: 800 DWight Way
STREET: 800 DWight Way
STREET: 800 DWight Way
STREET: 800 DWight Way
STREET: 0211fornia
COMPURPY: 0.5A
ZIP: 94701-1986
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb_Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb_Storage
COMPUTER: IBM
COMPUTER: DISKETTE, 1.5A
COMPUTER: WANTER: WASTEM: DOS
SOFTWARE: WANTER: WORDER: 05/08/595,718A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/595,718A
FILING DATE:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Buetner, Joseph A.
APPLICANT: Dadd, Christopher A.
APPLICANT: Baumbach, George A.
APPLICANT: Hammond, David J.
TITLE OF INVENTION: Fibrinogen Binding Peptides
NUMBER OF SEQUENCES: 8
                                                                                       0; Mismatches
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WS-08-022-381A-17

WS-08-022-381A-17

Sequence 17, Application US/08022381A

Fatent No. 5478810

GENERAL INFORMATION:

APPLICANT: Stuber, Werner

APPLICANT: Stuber, Werner

TITLE OF INVENTION: Peptide Amides, Processes for the

TITLE OF INVENTION: Preparation Thereof and Agents Containing These as

TITLE OF INVENTION: Preparation Thereof and Agents Containing These as

TITLE OF INVENTION: Preparation Thereof and Agents Containing These as

TITLE OF INVENTION: Preparation Thereof and Agents Containing These as

MUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W., Suite 700
                           APPLICANT: Stuber, Werner
APPLICANT: Stuber, Karl
APPLICANT: Stokenscher, Karl
TITLE OF INVENTION: Peptide Amides, Processes for the
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
TITLE OF INVENTION: Preparation Thereof and Agents Containing These as
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Punner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 1; Length 6; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC
COUNTRY: USA
ZUDY: USA
ZUDY: 20005-3115
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,381A
FLING DATE: 24-FEB-1993
CLASSIFICATION NUMBER: US 07/696,085
FLING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1991
APPLICATION NUMBER: US 07/696,085
FILING DATE: 06-MAY-1990
ATTORNEY/AGENT INPORMATION:
ANAME: ASSANCHION NUMBER: US 06-MAY-1990
ATTORNEY/AGENT INPORMATION:
ANAME: ASSANCHION NUMBER: US 06-MAY-1990
ATTORNEY/AGENT INPORMATION:
ANAME: ASSANCHION NUMBER: US 06-MAY-1990
ATTORNEY/AGENT INPORMATION:
ANAME: ASSANCHION:
ANAME: ASSANCHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MAIKOWICZ, KAIEN R.
REGISTRATION NUMBER: 36,351
REPERENCE PLOCKET NUMBER: 05552.1054-01000
TRIECOMMUNICATION INFORMATION:
TELEPHONE: 202,408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 4; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
3Y: linear
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COUNTRY: USA
ZIP: 20005-3315
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-022-381A-16
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APPLICANT: Baumbach, George A. APPLICANT: Hammond, David J.
APPLICANT: Hammond, David J.
APPLICANT: Lang, John M.
APPLICANT: Lang, John M.
APPLICANT: Galloway, Cynthia J.
TITLE OF INVENTION: Selective Stabilization of Protein TITLE OF INVENTION: During Viral Inactivation NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation STREET: 80 Obvight Way STREET: 80 Obvight Way STREET: 90 Obvight Way STREET: 90 Obvight Way STREET: 91 Obvight Way STREET: 90 Obvight Way STREET: 90 Obvight Way STREET: 80 Obvight W
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                                                                                   Query Match 100.0%; Score 25; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
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US-08-022-381A-16
US-08-021-916, Application US/08022381A
; Patent No. 5478810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/08672255
; Patent No. 5786458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single strand
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SEQUENCE CHARACTERISTICS:
LENGTH: 5
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Best Local Similarity 100.
Matches 4; Conservative
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STRANDEDNESS: sir
TOPOLOGY: linear
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    US-08-595-718A-4
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US-08-672-255-1
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Patent No. 5478810
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Fickenscher, Karl
TILLE OF INVENITION: Peptide Amides, Processes for the
TILLE OF INVENITION: Preparation Thereof and Agents Containing These as
TITLE OF INVENITION: Fibrin/Thrombin Clotting Inhibitors
UNUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: Dunner
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ZIP: DC
COUNTRY: USA
ZIP: 20005-3115
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELD FOCOMPATIBLE
COMPUTER: PACPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PACPATION BOTA:
SOFTWARE: PACPATION DATA:
APPLICATION NUMBER: US/08/022,381A
FLING DATE: 24-FEB-1993
CLASSIFICATION NUMBER: US 07/696,085
FLING DATE: 06-MAY-1991
PRIOR APPLICATION NUMBER: DE 40 14 655.3
FLING DATE: 08-MAY-1991
APPLICATION NUMBER: DE 40 14 655.3
FLING DATE: 08-MAY-1991
APPLICATION NUMBER: DE 40 18 655.3
FLING DATE: 08-MAY-1990
ATTELECOMMUNICATION NUMBER: 0552.1054-01000
TELECOMMUNICATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 36,351
                  NAME: Markowicz, Karen R.
REGISTRATION NUMBER: 36,351
REFRENCE/DOCKET NUMBER: 0552.1054-01000
TELEPHONE: 202-408-400
TELEPHONE: 202-408-400
INFORMATION OR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 25; DB 1;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0
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ATTORNEY/AGENT INFORMATION:
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202-408-4400
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                    amino acid
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3Y: linear
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Query Match 100.0%; Score 25; DB 1; Length 6; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
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Search completed: September 7, 2004, 19:01:24 Job time : 32 secs

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Sequence 16, Appli Sequence 2, Appli Sequence 25, Appli Sequence 25, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 28, Appli Sequence 28, Appli Sequence 3, Appli Sequence 3, Appli Sequence 8, Appli Sequence 138, App Sequence 49, Appl 7, 2004, 19:00:58; Search time 124 Seconds (without alignments) 10.163 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution. Description Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT They PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT They PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:* GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 0 US-09-779-054-16 0 US-09-931-009A-2 4 US-10-016-801-6 5 US-10-016-569A-25 5 US-10-308-644-25 8 US-10-308-644-25 10 US-10-619-520-2 2 US-10-619-520-2 2 US-10-619-520-2 2 US-10-414-524-28 5 US-10-449-659-14 10 US-10-449-659-14 10 US-10-334-726-138 2 US-10-334-726-138 1 US-10-283-429 Total number of hits satisfying chosen parameters: 1298764 seqs, 315065143 residues SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65 summaries OM protein - protein search, using sw model Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0
Maximum DB seq length: 2000000000 US-09-931-009A-2 25 1 GPRP 4 Query Match Length DB September BLOSUM62 100.0 Scoring table: Perfect score: Score Database : Sequence: Searched: Run on: Title: Result

equence 117, Appequence 49, Appequence 14, Appequence 117, Appequence 117, Appequence 117, Appequence 117, Appequence 12, Applequence 13, Appequence 12, Applequence 13, Applequence 12, Applequence 14, Apple	282 272 28, 113, 336
US-10-283-423-117 US-10-213-821-49 US-10-736-048-49 US-10-736-048-117 US-10-736-048-117 US-09-765-614B-110 US-09-765-614B-110 US-09-972-404B-23 US-09-972-404B-23 US-10-101-181-684-35 US-10-101-181-684-35 US-10-101-181-684-35 US-10-101-181-684-35 US-10-101-181-684-35 US-10-101-181-684-35 US-09-864-761-3365 US-09-833-285-94 US-09-833-285-94 US-09-833-285-94 US-09-833-285-94 US-09-833-285-94 US-09-833-285-94 US-09-833-285-94 US-09-833-285-94 US-09-833-285-94 US-09-833-285-94 US-09-844-761-8611-04 US-10-177-257-2 US-09-95-432A-5 US-09-95-432A-5 US-09-95-432A-5 US-09-95-432A-5 US-09-95-432A-5 US-09-95-432A-5 US-09-95-432A-5 US-09-964-761-6611-04 US-10-311-411-104 US-10-311-411-104 US-10-311-411-104 US-10-361-811-293 US-09-864-761-4736 US-09-864-761-4736 US-09-801-988-191-69	10-029-386-280 10-424-599-277 10-424-599-277 10-424-399-285 9-730-3798-3 9-864-761-3368 10-029-386-318
	14078888
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ALIGNMENTS

RESULT 1
US-09-779-054-16
Sequence 16, Application US/09779054
Sequence 16, Application US/09779054
Sequence 16, Application US/09779054
Sequence 16, Application US/09779054
Sequence 16, Application US
Sequence 10, US
Sequence 16, Application US
Sequence 10, US

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Sequence 25, Application US/10308644

Publication No. US20030229017A1

GENERAL INFORMATION:
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                                                                                                                  Sequence 25, Application US/10016569A

Sequence 25, Application US/20013A1

Sequence 25, Application NO. US20030229013A1

PUDLICANT: Nu, Shih-Kwang

APPLICANT: Teng, Chin-Lu

APPLICANT: Chang, Ting-Gung

TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing

TITLE OF INVENTION: the Same

FILE REPERENCE: P1379

CURRENT FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.2
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100.0%; Pred. No. 1.2e+06;
iive 0; Mismatches 0;
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US-09-953-657-4
GENERAL INFORMATION:
, APPLICANT: Buettner, Joseph A.
, APPLICANT: Buettner, Joseph A.
Baumbach, George A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.v
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ORGANISM: Human Cell
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US-10-308-644-25
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; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1el Sequenc
US-10-046-801-6
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US-10-046-801-6

Sequence 6, Application US/10046801

Publication No. US20030054027A1

GENERAL INFORMATION:

APPLICANT: Unger, Evan C.

TITLE OF INVENTION: Charged Lipids and Uses For The Same FILE REFERENCE: UNGRESS

CURRENT APPLICATION WIMBER: US/046,801

CURRENT APPLICATION WIMBER: US/09/540,448

PRIOR PILING DATE: 2002-05-13

PRIOR PILING DATE: 1997-09-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 6

LENTIN: 4
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100.0%; Score 25; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                             Similarity 100.0%; Score 25; DB 9; Length 4; Similarity 100.0%; Pred. No. 1.2e+06; 4; Conservative 0; Mismatches 0; Indels
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Sequence 2, Application US/09931009A

Publication No. US20330109431A1

GENERAL INFORMATION:

TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE

FILE REFERENCE: US 1257/01 (VA)

CURRENT APPLICATION NUMBER: US/09/931,009A

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 2

LENGTH: 4
                                                                    ; OTHER INFORMATION: thrombin-binding sequence US-09-779-054-16
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                 Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                        Query Match
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Sequence 2, Application US/10619520
Sequence 2, Application US/10619520
GENERAL INFORMATION:
APPLICANT: Richer, W.
APPLICANT: Schoppe, W.
TITLE OF INVENTION: ASENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DISFIGNATION: ASENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DISFIGNATION: ASENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DISFIGNATION NUMBER: US/10/619,520
CURRENT APPLICATION NUMBER: US/10/619,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-414-523-23
is Sequence 23, Application US/10414523
j Sequence 23, Application No. US20030211471A1
j GENERAL INFORMATION:
APPLICANT: Hammond, David J.
TILLE OF INVENTION: METHOD FOR DETECTING LIGANDS AND TARGETS IN A MIXTURE FILE REFERENCE: 221429
CURRENT APPLICATION NUMBER: US/10/414,523
CURRENT FILING DATE: 2002-04-14
PRIOR FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 6
MANAGER PATENT OF SEQ ID NOS: 23
SEQ ID NO 23
SEQ ID NO 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%; Score 25; DB 12; Similarity 100.0%; Pred. No. 1.2e+06; 4; Conservative 0; Mismatches 0;
                                                                        100.0%; Score 25; DB 12; 100.0%; Pred. No. 1.2e+06;
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Pred. No. 1.2e+06;
                                                                                                                     0; Mismatches
; OTHER INFORMATION: Synthesized Peptide US-10-619-520-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Synthesized Peptide
US-10-619-520-2
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SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 5
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                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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US-10-619-520-2
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Sublication No. US20040057957A1
GENERAL INFORMATION:
BAPPLICANT: Richer, W.
APPLICANT: Richer, W.
APPLICANT: Richer, W.
APPLICANT: Bieber, Franz
APPLICANT: Bieber, Franz
APPLICANT: Bieber, W.
TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DI FILE REFERENCE: Attorney Docket No. US20040057957A1 1328/2
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
COMPUTER: Diskette, 3.50 inch, 1.44Mb Storage
COMPUTER: Diskette, 3.50 inch, 1.44Mb Storage
COMPUTER: IBM
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 6.1
CURSUT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,657
FILING DATE: 17-Sep-2001
CLASSIFICATION: -UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/595,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

100.0%; Score 25; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
Hammond, David J.

TITLE OF INVENTION: Fibrinogen Binding Peptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 800 Dwight Way
P. O. Box 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: GIblin, James A.
REGISTRATION NUMBER: 25772
REFERENCE/DOCKET NUMBER: MSB-7233
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATE: 28-JUN-1990
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-953-657-4
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NAME/KEX: PEPTIDE
LOCATION: (1). (5)
OTHER INFORMATION: X is any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (510) 705-7910
TELEFAX: (510) 705-7904
JOURNAL: Thromb. Haemos
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ORGANISM: Artificial Sequence
                                                                                                                                                                CITY: Berkeley
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE LOCATION: (1)..(5)
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1 GPRP 4
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US-10-619-520-8
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APPLICANT: Raemussen, Fred H.
APPLICANT: Raemussen, Fred H.
APPLICANT: Raemussen, Fred H.
TITLE OF INVENTION: Assays for measuring matrix metalloproteinase activities
FILE REFERENCE: 56016-5001-US
CURRENT APPLICATION NUMBER: US/10/449,659
CURRENT APPLICATION NUMBER: US 60/384,135
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
LENGTH: 7
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0; Indels
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                                                                                                                                                            Sequence 28, Application US/10414524
| Publication No. US2003021253A1
| GENERAL INFORMATION:
| APPLICANT: Harmond et al.
| TILLE OF INVENTION: PLASMA PROTEIN-BINDING LIGANDS
| FILE REFERENCE: 221948
| CURRENT APPLICATION NUMBER: US/10/414,524
| CURRENT APPLICATION NUMBER: 60/372,091
| PRIOR FILING DATE: 2002-04-15
| NUMBER OF SEQ ID NOS: 119
| SOFTWARE: Patentin version 3.2
| LENGTH: 6
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100.0%; Score 25; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: metalloproteinase substrate US-10-449-659-14
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 14, Application US/10449659; Publication No. US20030229005A1
GENERAL INFORMATION:
APPLICANT: Cognosci, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), OTHER INFORMATION: Synthetic US-10-414-524-28
  4; Conservative
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1 GPRP 4
                                      1 GPRP 4
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US-10-414-524-28
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US-10-449-659-14
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  Matches
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RESULT 12

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APPLICANT: Richter, W.
APPLICANT: Richter, W.
APPLICANT: Bieber, Franz
APPLICANT: Bieber, Franz
APPLICANT: Bieber, Franz
APPLICANT: Tachoppe, W.
TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
FILE REFERENCE: Attorney Docket No. US20040057957A1 1328/2
CURRENT APPLICATION NUMBER: US/10/619,520
CURRENT APPLICATION NUMBER: US/10/619,520
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
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## Sequence 3, Application US/09730379B |
## Patent No. US20010044670A1 |
## Patent No. US20010044670A1 |
## Patent No. US20010044670A1 |
## PAPLICANT: Simantov M.D., Roy L. RAPLICANT: Simantov M.D., Roy L. RAPLICANT: Simantov M.D., Roy L. TITLE OF INVENTION: GLYCOPROTEIN AND METHODS OF USE |
## TITLE OF INVENTION: THROMBOSPONDIN BINDING REGION OF HISTIDINE-RICH |
## TITLE OF INVENTION: THROMBOSPONDIN BINDING REGION OF HISTIDINE-RICH |
## TITLE OF INVENTION: THROMBOSPONDIN BINDING REGION OF HISTIDINE-RICH |
## TITLE OF INVENTION: DATE: 2000-12-05 |
## TOWRENT FILING DATE: 2000-12-05 |
## TOWNSER OF SEQ ID NOS: 13 |
## SOFTWARE: Patentin Ver. 2.1 |
## SEG ID NO 3 |
## TYPE: PRT |
## ORGANISM: Homo sapiens |
## OURUME: 25 |
## TOWNSER: SEC ID NOS: 12 |
## TOWNSER: PATENTION BINDING REGION OF HISTIDINE-RICH |
## OURUME: 25 |
## TOWNSER: PATENTION BINDING REGION OF HISTIDINE-RICH |
## OURUME: 25 |
## TOWNSER: PATENTION BINDING REGION OF HISTIDINE-RICH |
## OURUME: 25 |
## TOWNSER: PATENTION BINDING REGION OF HISTIDINE-RICH |
## OURUME: 25 |
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## OURUME: 25 |
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100.0%; Score 25; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.2e+06;
Conservative 0; Mismatches 0;
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PAGES: 2220-225
DATE: 1986
PUBLICATION INFORMATION: PUBLICATION INFORMATION
JOURNAL: Blochemistry
VOLUME: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DATABASE ACCESSION NUMBER: Genbank/P04196
US-09-730-379B-3
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NAME/KRY: PEPTIDE
NOCATION: (1)..(9)
FEATURE:
NAME/KRY: PEPTIDE
NAME/KRY: PEPTIDE
NOCATION: (1)..(9)
OTHER INFORMATION: Synthesized Peptide
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APPLICANT: Robert, Koll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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Sequence 117, Application US/10283423

| Sequence 117, Application No. US203316223A1
| GENERAL INFORMATION:
| APPLICANT: Lowerty, David E. APPLICANT: Swith, Valdin G. APPLICANT: Expersen, Martha J. TITLE OF INVENTION: Droscophila G Protein Coupled Receptors, Nucleic Acids, And Methods TITLE OF INVENTION: Related To The Same
| FILE REFERENCE: PHRM0002-102 | APPLICATION | Project
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APPLICANT: Marthaudin G.
APPLICANT: Subject G.
APPLICANT: Subject G.
APPLICANT: Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods TITLE OF INVENTION: Related To The Same FILE REFERENCE: 6297.2cp
CURRENT APPLICATION NUMBER: US/10/213,821
CURRENT APPLICATION NUMBER: 09/693,746
PRIOR FILING DATE: 2000-10-20
PRIOR PRILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 185
SOFTWARE PATENTIAN VERSION 3.1
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PRIOR FILING DATE: PriorFilingDate: 2000-10-20
PRIOR APPLICATION NUMBER: PriorAppNumber: 09/425,676
PRIOR FILING DATE: PriorFilingDate: 1999-10-22
NUMBER: OF SEQ ID NOS: 187
SCFTWARE: Patentin version 3.2
SEQ ID NO II D NO II
           Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 4; Conservative 0; Mismatches 0;
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CTHER INFORMATION: No. US20030162223Alel Sequence US-10-283-423-117
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-10-30
Earlier Applications
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Publication No. US20030180297A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-10-213-821-49
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US-10-283-423-49
US-10-283-423-49
Sequence 49, Application US/10283423
Publication No. US20030162223A1
GENERAL INFORMATION:
APPLICANT: Lowery, David E.
APPLICANT: Smith, Valdin G.
APPLICANT: Michaek, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: Belated To The Same
TITLE OF INVENTION: Related To The Same
FILE REFERENCE: PHRM0002-102
FILE REFERENCE: PHRM0002-102
Application Project
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PRIOR FILING DATE: PriorFilingDate: 2000-10-20
PRIOR APPLICATION NUMBER: PriorAppNumber: 09/425,676
PRIOR FILING DATE: PriorFilingDate: 1999-10-22
NUMBER OF SEQ ID NOS: 187
SOFTWARE: Patentin version 3.2
SEQ ID NO 49
LENGTH: 9
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US-10-283-423-49
                                                                                                                                                                                                Sequence 138, Application US/10334726
Publication No. US20030211521A1
GENERAL INFORMATION:
APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
TITLE OF INVENTION: BREAST CANCER ANTIGEN
FILE REPERENCE: 1090-36
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US/09/645,446
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 1990-03-19
PRIOR FILING DATE: 1990-03-19
PRIOR FILING DATE: 1998-09-20
PRIOR FILING DATE: 1998-09-20
PRIOR FILING DATE: 1998-09-20
SOFTWARE: PatentIn Ver. 2.0
SSOFTWARE: PatentIn Ver. 2.0
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CURRENT FILING DATE: 2002-10-30
Earlier Applications
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 4; Conserv
GPRP 4
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APPLICANT: Lowery, David E. APPLICANT: Smith, Valdin G. APPLICANT: Smith, Valdin G. APPLICANT: Smith, Valdin G. APPLICANT: Smith, Valdin G. APPLICANT: Rubiak, Teresa M. APPLICANT: Rubiak, Teresa M. APPLICANT: Largesh, Martha J. TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acide, And Methode TITLE OF INVENTION: Related To The Same TITLE OF INVENTION: Related To The Same CURRENT APPLICATION NUMBER: US/10/736,048
CURRENT FILING DATE: 2000-10-20
PRICE FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 168
SOFTWARE: Patentin Version 3.1
SEQ ID NO 117
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; Sequence 10, Application US/09765614B
; Retent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; TITLE OF INVENTION: agents
; TITLE OF INVENTION: agents
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT PILING DATE: 2001-07-10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
LENGTH: 10
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
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; Sequence 117, Application US/10736048
; Publication No. US20040121956A1
; GENERAL INFORMATION:
                                                                                                                                   OTHER INFORMATION: Novel Sequence
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ORGANISM: Artificial Sequence
PEATURE:
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                                       TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 9
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US-10-
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APPLICANT: David E.
APPLICANT: David E.
APPLICANT: David E.
APPLICANT: Smith, Valdin G.
APPLICANT: Larsen, Martha J.
APPLICANT: Larsen, Martha J.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
TITLE OF INVENTION: Related To The Same
FILE REFERENCE: 6297.20p
CURRENT APPLICATION NUMBER: US/10/213, 821
CURRENT PILING DATE: 2003-01-21
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 185
SOFTWARE: Patentin version 3.1
LENGTH: 9
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100.0%; Pred. No. 1.2e+06;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
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                                                                              OTHER INFORMATION: No. US20030180297Alel Sequence
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o. US20030180297A1
          ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Publication No. US20
GENERAL INFORMATION
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US-09-572-404B-230
; Sequence 230, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REPERENCE: Human patent
; CURRENT APPLICANTION NUMBER: US/09/572,404B
; CURRENT PILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SQOTWARE: ProtPatent version 1.0
; LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09925715
Patent No. US20020102217A1
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/206
CURRENT APPLICATION NUMBER: US/09/925,715
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 7
LENGTH: 10
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OTHER INFORMATION: Description of Artificial Sequence:Biotinylated OTHER INFORMATION: fibrin-antipolymerant peptide
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Biotin-Gly
NAME/KEY: MOD RES
LOCATION: (10)
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CTHER INFORMATION: Sequence:Biotinylated
CTHER INFORMATION: fibrin-anti-polymerant peptide
NAME/KEY: MOD_RES
LOCATION: (1)
CTHER INFORMATION: Biotinylated-Gly
NAME/KEY: MOD_RES
LOCATION: (10)
CTHER INFORMATION: AMIDATION
US-09-765-6148-10
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100.0%; Score 25; DB 9; 1
Best Local Similarity 100.0%; Pred./No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 4; Conservative
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ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                  1 GPRP 4
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US-09-925-715-7
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; OTHER INFORMATION: sequence located in MCP at 295-304 and may interact with Sequence; CTHER INFORMATION: this patent.
US-09-572-404B-230
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US-10-151-82-28
Sequence 28, Application US/10151882
| Publication No. US20030059862A1
| GENERAL INFORMATION:
| APPLICANT: Richen, Steven M. |
| TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
| TITLE OF INVENTION: ANTIBODIES: US/10/151,882
| CURRENT FILING DATE: 2002-05-22
| CURRENT FILING DATE: 2001-05-24
| NUMBER OF SEQ ID NOS: 48
| SOFTWARE: Patentin Version 3.0
| SEQ ID NO 28
| LENGTH: 10
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0
                                                                                                                 Query Match
100.0%; Score 25; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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US-10-076-547-10
is Sequence 10, Application US/10078547
is Bublication Wo. US20020199211A1
is GENERAL INFORMATION:
APPLICANT: Marayanaswamy Ramesh
APPLICANT: Miguel A. de la Fuente
APPLICANT: Ines M. Anton
ITLE OF INVENTION: WIP, A WASP-Associated Protein
FILE OF INVENTION: WIP, A WASP-Associated Protein
FILE REFERENCE: 1242.1022-005
CURRENT APPLICATION NUMBER: 09/599.287
PRIOR APPLICATION NUMBER: 09/599.287
PRIOR APPLICATION NUMBER: 09/599.287
PRIOR APPLICATION NUMBER: 60/101,457
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 27
SOFTWARR: FARENCE OF OF Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: WIP sequence 410-419 a.a., human
US-10-078-547-10
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100.0%; Score 25; DB 13;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0;
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US-10-151-882-28
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Query Match 100.0%; Score 25; DB 13; Length 15; Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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Similarity 100.0%; Pred. No. 5.9e+02;
4; Conservative 0; Mismatata
                                                                                                                                                                                                                                                                                                               APPLICANT: RAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dans M.
APPLICANT: FOWLKES, Dans M.
APPLICANT: STIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SUCHNOCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICALLO...
PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FBB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. LESLIGE
REGISTRATION NUMBER: 1101-202
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPROMINE: (212) 790-9090
"THE TELEPROMINE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                     Sequence 411, Application US/10161791
Publication No. US20030186863A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // Sequence 3, Application US/10177257
// Publication No. US20030082768A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENUE
INFORMATION FOR SEQ ID NO: 411:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-10-161-791-411
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: SPARKS
                                                                                                                                    7 GPRP 10
                                                                                             1 GPRP 4
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US-10-177-257-3
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; Sequence 3. Application US/10068569
; Publication No. US2002016097541
; GENERAL INFORMATION:
    APPLICANT: Srinivasula, Srinivasa M.
    APPLICANT: Fernandee-Alnemri, Teresa
    APPLICANT: Alnemri, Emad S.
    TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
    TITLE OF INVENTION: A CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
    TURENT FILING DATE: 202-02-06
    NUMBER OF SEQ ID NOS: 28
    SOFTWARE: PastSEQ for Windows Version 4.0
    SEQ ID NO 5
    LENGTH: 15
                                                Gaps
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Query Match
100.0%; Score 25; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Sequence 10, Application US/10722075

Publication No. US2004014192A1

GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: diagnostic/therapeutic
TITLE OF INVENTION: diagnostic/therapeutic
TITLE OF INVENTION: agents // 10722,075

FILE REFREENCE: REF/Klaveness/054

CURRENT APPLICATION WHERE: US/10/722,075

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: US/08/960,054A

PRIOR APPLICATION NUMBER: US/08/960,054A

PRIOR APPLICATION NUMBER: US/08/960,054A

PRIOR SEQ ID NOS: 31

SOFTWARE: PATENTE: 1997-10-29

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 10

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence: Botinnylated
OTHER INFORMATION: fibrin-anti-polymerant peptide
FEATURE:
NAMEK KEY: MOD RES
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100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (10)
OTHER INFORMATION: AMIDATION
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Best Local Similarity 100..
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JS-10-068-569-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD RES
LOCATION: (10)
                                                                                           1 GPRP 4
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RESULT 31

US-10-181-654-21

US-10-181-654-21

US-10-181-654-21

Sequence 21, Application US/10181654

Publication No. US2003108957A1

GENERAL INFORMATION:

APPLICANT: The Wister Institute of Anatomy and Biology

APPLICANT: The Wister Institute of Anatomy and Biology

APPLICANT: Blaszzyk-Thurin, Magdalena

APPLICANT: Blaszzyk-Thurin, Magdalena

APPLICANT: Blaszzyk-Thurin, Magdalena

APPLICANT: Blovas, Sandor

TITLE OF INVENTION: Use

FILE REFERENCE: WF94BPCT

CURRENT FILING DATE: 2002-07-19

FRIOR APPLICATION NUMBER: US 60/177,565

PRIOR APPLICATION NUMBER: US 60/237,599

FRIOR PILING DATE: 2000-10-21

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 36

SEQ ID NO 21

LENGTH: 18

WUNDER OF LENGTH: 18

LENGTH: 18

WORDEN OF LENGTH: 18
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; Sequence 35, Application US/10181654
; Publication No. US20030108957A1
; Publication No. US20030108957A1
; GENERAL INFORMATION:
; APPLICANT: The Wister Institute of Anatomy and Biology
; APPLICANT: Creighton University
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Lovas, Sandor
; APPLICANT: Lovas, Sandor
; TITLE OF INVENTION: Biocidal Molecules, Macromolecular Targets and Methods of Producti
; CURRENT APPLICATION NUMBER: US/10/181,654
; CURRENT APPLICATION NUMBER: US 60/177,565
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                          Query Match
100.0%; Score 25; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                               STRANDEDNESS: single
STRANDEDNESS: single
COPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-09-805-301-92
     INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-181-654-21
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APPLICANT: Baskerville, Donald Scott
APPLICANT: Bartel, David P.
TITLE OF INVENTION: Use of a Ribozyme to Join Nucleic Acids
TITLE OF INVENTION: use of a Ribozyme to Join Nucleic Acids
TITLE OF INVENTION: und Peptides
FILE REPRENCE: 0399.1177.007
CURRENT APPLICATION NUMBER: US/10/177,257
CURRENT FILING DATE: 2002-06-20
FRIOR PEPLICATION NUMBER: US/09/702,543
FRIOR FILING DATE: 1999-04-14
FRIOR APPLICATION NUMBER: US 60/082,256
FRIOR APPLICATION NUMBER: US 60/082,256
FRIOR RELING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 25; DB 14; Length 17; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Comparible
OPERATING SYSTEM: IBM D.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIPFICATION ** CURKNOWN>
PRIOR APPLICATION ATA:
APPLICATION DATA:
APPLICATION TOWNER: 08/584,043
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
RESTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92, Application US/09805301
Patent No. US20020173456A1
GENERAL INFORMATION:
SPATICANI: Sparrow, James T.
HAUBER, Jochen
Mims, Marcha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90701-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: BIV-1 Tat peptide
US-10-177-257-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 139
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glema C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION WIMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION WUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
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                                                                                                                                    NY: EXPRESSED IN PLACENTA, SIGNAL = 2.7

NY: EXPRESSED IN PLACENTA, SIGNAL = 2.9

NY: EXPRESSED IN BOYE WARROW, SIGNAL = 2.5

NY: EXPRESSED IN PETAL LIVER, SIGNAL = 2.6

NY: EXPRESSED IN HELA, SIGNAL = 2.6

NY: EXPRESSED IN HELA, SIGNAL = 2.1

NY: EXPRESSED IN HELA, SIGNAL = 2.1

NY: EXPRESSED IN HEART, SIGNAL = 2.1

NY: EXPRESSED IN HEARY, SIGNAL = 2.1

NY: EXPRESSED IN HELIOO, SIGNAL = 2.6

NY: EXPRESSED IN HELIOO, SIGNAL = 2.6

NY: EXPRESSED IN HELIOO, SIGNAL = 2.4

NY: EXPRESSED IN HELIOO, SIGNAL = 2.4

NY: EXPRESSED IN HELIOO, SIGNAL = 2.4

NY: EXT HUMAN HIT: W529911, EVALUE 1.10e-01

NY: EXT HUMAN HIT: AM95693511, EVALUE 7.60e-02
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APPLICANT: Kongsuwan, Kriteaya
APPLICANT: Wijffels, Gene L.
APPLICANT: Wijffels, Philip A.
APPLICANT: Kemp, Gregory W.
TITLE OF INVENTION: WETHOD OF IDENTIFYING ANTIBACTERIAL
TITLE OF INVENTION:
FILE REFERENCE: CULLN42.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 25; DB 9; ]; Pred. No. 7.1e+02; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1348, Application US/10225567A Publication to US20030113798A1 GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 102, Application US/10416249 Publication No. US20040132121A1 GENERAL INFORMATION:
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100.0%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1348
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-1348
                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                 FEATURE:
OTHER INFORMATION: M.
OTHER INFORMATION: E.
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CTHER INFORMATION:
CTHER INFORMATION:
US-09-864-761-33658
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      LENGTH: 20
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100.0%; Score 25; DB 14; 1
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0;
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SEQ ID NO 33658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 50/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-07
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-01-21
PRIOR PELICATION NUMBER: US 60/237,599
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
SEQ ID NO 35
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33658, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                , TYPE: PRT
, ORGANISM: Apidaecin la
US-10-181-654-35
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                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 25; DB 11; Length 2:
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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US-10-373-809-94

§ Gequence 94, Application US/10373809

§ bublication No. US20040023260A1

§ GENERAL INFORMATION:

§ TITLE OF INVENTION: 29 Human Secreted Proteins

FILE REFERENCE: PZ015P1

CURRENT APPLICATION NUMBER: US/10/373,809

CURRENT FILING DATE: 2003-02-27

PRIOR APPLICATION NUMBER: US/09/729,835

PRIOR APPLICATION NUMBER: 09/257,179

PRIOR FILING DATE: 1999-02-25

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/056,270

PRIOR APPLICATION NUMBER: 60/056,271

PRIOR APPLICATION NUMBER: 60/056,271

PRIOR FILING DATE: 1997-08-29

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PALENTIN VET: 2.0
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Publication No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: THAIL J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: STUESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT WUERHOFF
  PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-1
PRIOR PELING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SEQ ID NO 551
LENGTH: 21
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US-10-373-809-94
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; ORGANISM: Homo sapiens
US-09-833-245-551
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8 GPRP 11
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US-08-424-550B-415
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100.0%; Score 25; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Sequence 94, Application US/09729835

Sequence 94, Application US/09729835

GENERAL INFORMATION:

APPLICATUR: Ruben et al.

TITLE OF INVENTION: 29 Human Secreted Proteins

FILE REPRENCE: PSOLSFI

CURRENT APPLICATION NUMBER: US/09/729,835

CURRENT FILING DATE: 2000-12-06

PRIOR APPLICATION NUMBER: 09/257,179

PRIOR APPLICATION NUMBER: 60/056,270

PRIOR PRILING DATE: 1997-08-29

PRIOR FILING DATE: 1997-08-29

PRIOR FILING DATE: 1997-08-29

PRIOR APPLICATION NUMBER: 60/056,271

PRIOR APPLICATION NUMBER: 60/056,073

PRIOR FILING DATE: 1997-08-29

PRIOR FILING DATE: 1997-08-29

PRIOR FILING DATE: 1997-08-29

PRIOR FILING DATE: 1997-08-29

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PATCHIN VOR: 2.0
CURRENT APPLICATION NUMBER: US/10/416,249
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: PCT/AU01/01436
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
SPRIOR FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 678
SOFTWARE: PASESEQ for Windows Version 4.0
SCOTTANTE: 20
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Publication No. US20040010134A1
GENERAL INFORMATION:
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FOT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT

; ORGANISM: Magnetospirillum magnetotacticum

1; 10-416-249-102
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US-09-729-835-94
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US-09-833-245-551
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-03-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 470
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 323, Application US/03397945
Publication No. US20030065139A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
ITILE OF INVENTION: 95 Human secreted proteins
CURRENT APPLICATION NUMBER: US/09/397,945
CURRENT FILING DATE: 1999-09-17
PRIOR PILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR PILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 25; DB 12;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 7.7e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-10-653-595-323
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; ORGANISM: Homo sapiens
US-09-397-945-323
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Best Local Similarity
Matches 4; Conserv
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APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJAK
APPLICANT: SISA K. WUSHAHWAR
ITILE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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100.0%; Pred. No. 7.7e+02;
Five 0: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
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Sequence 323, Application US/10653595

Publication No. US20040048304A1

GENERAL INPORMATION:

APPLICANT: Ruben et. al.

TITLE OF INVENTION: 95 Human secreted proteins

FILE REPERENCE: PZ027PIC1

CURRENT APPLICATION NUMBER: US 09/397945

PRIOR FILING DATE: 1999-03-17

PRIOR APPLICATION NUMBER: US 09/397945

PRIOR FILING DATE: 1999-03-18

PRIOR APPLICATION NUMBER: 60/078,566

PRIOR APPLICATION NUMBER: 60/078,566

PRIOR FILING DATE: 1998-03-19

PRIOR FILING DATE: 1998-03-19

PRIOR FILING DATE: 1998-03-19

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: 60/078,574

PRIOR PILING DATE: 1998-03-19

PRIOR PILING DATE: 1998-03-19

PRIOR PILING DATE: 1998-03-19

PRIOR PILING DATE: 1998-03-19
                                                                                                                                                                                                  D377/AP6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFO TOTON:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                               ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-03-19
APPLICATION NUMBER: 60/080,314
FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/080,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 415:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435435
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-424-5508-415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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USA
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FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: SPAS-1 cDNA US-09-952-432A-5
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100.0%; Score 25; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                             Sequence 5. Application US/09952432A

Patent No. US2002015588A1

GENERAL INFORMATION:
APPLICANT: Alison, James P.
APPLICANT: Ansatri, Nilaba

APPLICANT: Shastri, Nilaba

APPLICANT: Shastri, Nilaba

APPLICANT: Shastri, Nilaba

TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN

TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN

FILE REFERENCE: 019941-0011003

CURRENT APPLICATION NUMBER: US/09/952,432A

CURRENT FILING DATE: 2002-04-15

PRIOR FILING DATE: 2000-09-21

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENTH: 24
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Sequence 104, Application US/09726643

Sequence 104, Application US/09726643

Sequence 104, Application US/09726643

GENERAL INCORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 26 Human secreted proteins

FILE REPREBUGE: PX040P1

CURRENT APPLICATION NUMBER: US/09/726,643

CURRENT PRIOR DATE: 2000-12-01

PRIOR FILING DATE: 2000-06-02

PRIOR APPLICATION NUMBER: 60/137,725

PRIOR APPLICATION NUMBER: 60/137,725

NUMBER OF SEQ ID NOS: 190

SEQ ID NOS: 190

SEQ ID NO 104

LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-09-726-643-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 GPRP 22
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US-09-864-761-36112
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JOHN TO SEQUENCE 1, Application US/1017257

Publication No. US20030082768A1

GENERAL INFORMATION:

APPLICANT: Barkerville, Donald Scott
APPLICANT: Barkerville, Donald Scott
APPLICANT: Barkerville, Donald Scott
APPLICANT: Barkerville, Donald Scott
TITLE OF INVENTION: Use of a Ribozyme to Join Nucleic Acids
TITLE OF INVENTION: and Peptides
FILE REFERENCE: 0399.1177-007

CURRENT APPLICATION NUMBER: US/09/702,543

PRIOR APPLICATION NUMBER: US/09/702,543

PRIOR APPLICATION NUMBER: US 60/082,256

PRIOR FILING DATE: 1999-04-14

PRIOR FILING DATE: 1999-04-17

PRIOR FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squence 2, Application US/1017257

Squence 2, Application US/1017257

Squence 2, Application Wo. US20308276841

GENERAL INFORMATION:

APPLICANT: Barkerville, Donald Scott

APPLICANT: Ware of a Ribozyme to Join Nucleic Acids

ITLE OF INVENTION: USe of a Ribozyme to Join Nucleic Acids

FILE REFERENCE: 0399-1177-007

CURRENT APPLICATION NUMBER: US/09/102,543

PRIOR FILING DATE: 1999-04-14

PRIOR APPLICATION NUMBER: US 60/082,256

PRIOR APPLICATION NUMBER: US 60/082,256

PRIOR PILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 23

TYDEN DEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 14; Length 23; 100.0%; Pred. No. 8e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 25; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Tat tag peptide 1 US-10-177-257-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Tat 2 tag peptide
US-10-177-257-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Unknown
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100.0%; Score 25; DB 9; Length 26; 100.0%; Pred. No. 8.9e+02; Live 0; Mismatches 0; Indels ; Sequence 36112, Application US/09864761; Patent No. US20020048763A1; GENERAL INFORMATION:

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Sequence 140, Application US/10001885

| Sequence 140, Application US/10001885
| Publication No. US20040058319A1
| GENERAL INFORMATION:
| APPLICANT: Salceda, Susana
| APPLICANT: Recipon, Herve
| APPLICANT: Recipon, Herve
| APPLICANT: Cafferkey, Robert
| APPLICANT: Cafferkey, Robert
| APPLICANT: Cafferkey, Robert
| APPLICANT: Liu, Yongming
| APPLICANT: Liu, Chenghua
| TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prot
| TILE OF INTENTION: Compositions and Methods Relating to Ovary Specific Genes and Prot
| TILE OF ILLNO DATE: 2001-11-20
| PRIOR PILIATION NUMBER: 60/252,061
| PRIOR PILIATION NUMBER: 60/252,061
| PRIOR PILIATION NUMBER: 60/253,257
| NUMBER OF SEQ ID NOS: 167
| SEQ ID NOS: 167
| SEQ ID NO 140
| LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 26;
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Pred. No. 8.9e+02;
; Mismatches 0;
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GENERAL INCLEAR:

TILLE OF INVENTION: 26 Human secreted proteins
FILE REPERENCE: P2040P1
FULE REPERENCE: P2040P1
CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR PILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PATENTIN UNE: 2.0
SOFTWARE: PATENTIN UNE: 2.0
SOFTWARE: PATENTIN UNE: 2.0
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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Best Local Similarity 100.
Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-10-042-141-104
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US-10-001-885-140
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US-10-042-141-104
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APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: HUMAN GENE CA.1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-06-37

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667
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D IN FETAL LIVER, SIGNAL = 1
D IN BONE MARROW, SIGNAL = 11
D IN HELLA, SIGNAL = 11
D IN HELLO, SIGNAL = 11
D IN BT474, SIGNAL = 34
D IN BTATIN, SIGNAL = 10
D IN BRAIN, SIGNAL = 10
D IN BRAIN, SIGNAL = 10
D IN LUNG, SIGNAL = 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00069
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 36112
PURNETH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO ALL18511.6
OTHER INFORMATION: EXPRESSED IN PLACENTY
OTHER INFORMATION: EXPRESSED IN HEART,
OTHER INFORMATION: EXPRESSED IN FETAL I
OTHER INFORMATION: EXPRESSED IN HEART,
OTHER INFORMATION: EXPRESSED IN HELA,
OTHER INFORMATION: EXPRESSED IN HELA,
OTHER INFORMATION: EXPRESSED IN B1100
OTHER INFORMATION: EXPRESSED IN B1100
OTHER INFORMATION: EXPRESSED IN B174,
OTHER INFORMATION: EXPRESSED IN B174,
OTHER INFORMATION: EXPRESSED IN B174,
OTHER INFORMATION: EXPRESSED IN B171,
OTHER INFORMATION: EXPRESSED IN B171,
OTHER INFORMATION: EXPRESSED IN LUNG,
US-09-864-761-36112
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Best Local Similarity
Matches 4; Conserv
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.. 0

Gaps

.; 0

0

Gaps .

; Sequence 12, Application US/10361848; Publication No. US20030221207A1

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GREENT INFORMATION:
APPLICAMT: MOMBADON BILD
TITLE OF INVENTION: DESTROCEMENT TYPE 2 TRANSCENIC MICE
FILE PERPERENCE: 06756.00463
CURRENT APPLICATION NUMBER: U5/10/361,048
NUMBER OF SEQ ID NOS: 310-02-11
NUMBER OF SEQ ID NOS: 310-02-11
SOCTUMARE: PERFECT OF WINDOWS: 310-001
SOCTUMARE: DESTRUCTION ONS: 310-001
SOCTUMARE: PERFECT OF MINDOWS VERSION 4.0
SOCTUMARE: PERFECT OF MINDOWS: 00 Mismatches 0; Indels 0; Gaps 0;
SOCTUMARE: PERFECT OF MINDOWS: 00 Mismatches 0; Indels 0; Gaps 0;
MATCHES OF 00 MISMATION: 00 MISMATION ON 00 MISMATCHES 0; Indels 0; Gaps 0;
MATCHES OF 00 MISMATION ON 00 MISMATION ON 00 MISMATCHES 0; Indels 0; Gaps 0;
MATCHES OF 00 MISMATION ON 00 MISMATCHES 0; Indels 0; Gaps 0; MISMATCHES 00 MISMATCHES 00; M
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Search completed: September 7, 2004, 19:12:28 Job time : 126 secs

18 GPRP 21

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2004, 18:45:11; Search time 123 Seconds

(without alignments)

9.189 Million cell updates/sec

Perfect score: 25

Perfect score: 25

Sequence: 1 GPRP 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries
Listing first 65 summaries

A_Geneseq_29dan(**
1: __geneseqp1990s:*
2: __geneseqp1990s:*
3: __geneseqp2001s:*
5: __geneseqp2001s:*
6: __geneseqp2003s:*
7: __geneseqp2003s:*
8: __geneseqp2003s:*
8: __geneseqp2003s:*
9: __geneseqp2003s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

726 Anticoa	724	3727 Anticoa	371	5718	333	330	334	863	570	188	868	897	1327	329	3733 Anticoa	3730 Anticoa	3731 Anticoa	3732 Anticoa	3729 Anticoa	332 Blood o	3982	3867 Fibrino	9979 Primate	3119	199 GPRP-pep	1606 Thrombi	1903	5504 TC-99m l	3469 Ligand #	1923	5519	3286	9317	2090	2903	5446	Ade25505 Tc-99m la	1924 Peptide	5517 Fibrin p
2 AAR157	2 AAR1572	2 AAR1572	2 AAR1571	2 AAR1571	2 AAR6033	2 AAR6033	2 AAR6033	2 AAW0986	2 AAW3457	2 AAW4718	2 AAW9289	2 AAW9289	5 AA01832	5 AA01832	2 AAR1573	2 AAR1573	2 AAR1573	2 AAR1573	2 AAR1572	2 AAR6033	3 AAY7898	8 ADE8686	7 ADD6997	2 AAR6931	2 AAW2519	2 AAW5060	2 AAW8790	2 ADE2550	2 ADE2546	3 AAY5492	3 AAY9551	6 ABU0828	2 AAR6931	2 AAW5060	2 AAW9290	2 AAY5544	9 2 ADE25505	3 AAY5492	3 AAY9551
5 100.	5 100.	5 100.	5 100.	100.	100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	5 100.	25 100.0	5 100.	5 100.
26	27	28	29	30	31	32	33	3.4	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	26	57	58	59	9	61	62	63	64	65

ALIGNMENTS

RESULT 1

744	22D61324
ដ	AAP61324 standard; peptide; 4 AA.
X	
AC	AAP61324;
×	
DŢ	
DŢ	
Į	03-OCT-2002 (revised)
I	
×	
SE SE	Sequence of tetrapeptide of desAA-fibrin.
₹ ₹	Tissue plasminoden activator: fibrinolysis: assay; diad
X	
SO	Coelognathus radiatus.
SO	Bothrops; genus".
×	
Md	WO8605814-A.
×	
PD	09-OCT-1986.
X	
PF	27-MAR-1986; 86WO-SE000144.
X	
PR	01-APR-1985; 85SE-00001614.
XX	
PA	
PA	(RANB/) RANBY M G.

N

us-09-931-009a-2.open.rag

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WPI; 1986-278827/42

Ranby M;

The patentors claim a compsn. in which AAP61324 is pref. present at a conc. of equal to or more than, 0.4 (pref. 2) mg./ml. of the compsn. The compsn. can be used in diagnostic tests such as the determ. of the enzyme tissue plasminogen activator as a standard in the detection of trace amts. of fibrin in biological fluids. It may also be administered in vivo to measure the total fibrinolytic capacity of an organism. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to standardise OS field) Fibrin solubilised with tetra:peptide - used in diagnostic procedures for determining fibrinolysis factors. Claim 2; Page 18; 22pp; English.

Sequence 4 AA;

Length 4; Query Match 100.0%; Score 25; DB 1; Lo Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; 1 GPRP 4 ઠે

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Gaps

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Indels

GPRP 4

AAR05320 standard; peptide; 4 AA. RESULT 2 AAR05320

(first entry) (revised) 25-MAR-2003 08-OCT-1990 AAR05320;

Anti-coagulant peptide

Anti-coagulant; cerebral thrombosis; myocardial infarction. Synthetic

/label= proline or prolylproline. Location/Qualifiers 'label= ornithine, Misc-difference Misc-difference

27-APR-1990

21-OCT-1988;

88JP-00265809

21-OCT-1988;

(DAUC) DAIICHI SEIYAKU

WPI; 1990-175285/23.

Peptide contg. proline - is used for cerebral thrombosis, myocardial infarction etc. due to anti-coagulation activity.

Claim 1; Page 975; 10pp; Japanese.

C-terminal is in amide form. (Updated on 25-MAR-2003 to correct PA

Sequence of peptide which binds to human fibrinogen.

Sequence 4 AA;

0 ô Synthetic peptides beginning with the sequence Gly-Pro-Arg (e.g. GPRP) will bind to fibrinogen and prevent fibrin polymerisation. A scrambling reaction was used to determine whether unique GPR-like peptides could be created from a reaction seeded with GPR if these new products could bind to fibrinogen. See e.g. AAR32379. (Updated on 25-MAR-2003 to correct Gaps Gaps platelet aggregation, fibrinogen A-alpha chain, protein scrambling, GPR-like peptide. Identifying peptide(s) which bond to predetermined targets - by degradation and recombination of peptide(s) and isolating bound . 0 ., Length 4; Length 4; Indels Indels 100.0%; Score 25; DB 2; L 100.0%; Pred. No. 1.4e+06; h Similarity 100.0%; Score 25; DB 2; L Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Ö Example 5; Page 58; 89pp; English. AAR32382 standard; peptide; 4 AA. AAR49796 standard; peptide; 4 AA Fibrinogen binding peptide #6. Ľ 92WO-US006933 91US-00813315 (revised)
(first entry) (revised)
(first entry) Venton DL, Hopfinger AJ, Conservative (RECE-) RECEPTOR LAB INC WPI; 1993-093932/11. Similarity Query Match Best Local Similarity Matches 4; Conserv 1 GPRP 4 Sequence 4 AA; 1 GPRP 1 GPRP WO9304079-A1 20-AUG-1992; 21-AUG-1991; 04-MAR-1993. 25-MAR-2003 01-JUL-1993 4, 25-MAR-2003 23-AUG-1994 peptide(s). Synthetic. PN field.) AAR32382; Query Match Best Local AAR49796; Matches AAR49796 g EXEEXAXE à 엄

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In the qualitative or quantitative determn. of thrombin-induced platelet aggregation in the presence of fibrin, interference from fibrin clot formation is suppressed with a fibrin-aggregation inhibitor (e.g., AAM09661-63). The assay may be used to determine the platelet aggregation inhibitory activity of thrombin inhibitors. The peptides inhibit fibrin clot formation at high thrombin concns. without inhibiting platelet
                                                                                                                                                              Determn. of thrombin-induced platelet aggregation in presence of fibr
comprises use of fibrin aggregation inhibitor to suppress fibrin clot
94EP-00119803.
                                93DE-04344919.
                                                                                                                                                                                                                                  Claim 4; Col 5; 5pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                (BEHW ) BEHRINGWERKE
                                                                                                                                  WPI; 1995-233339/31
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4 AA;
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15-DEC-1994;
                                30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                          aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                    Formation
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                                                                                                  Reers M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The inventors claim a method for inexpensively and rapidly producing a large and varied population of peptides and screening this varied population of peptides and screening this varied population for the presence of peptides which bind to a target, for example, a macromolecule associated with a particular physiological function. The specific binding peptides are isolated and sequenced, synthesised on a large-scale, their biological activity is demonstrated, and then subjected to clinical testing. The random population of peptides is generated by employing a scrambling system which utilises one or more proteases, esp. papain, pepsin, bromelin, thermolyshin, trypsin, promase, chymotrypsin, subtilism and dipeptidyl peptidase IV. A typical starting protein is casein. Targets are esp. receptors involved in physiological processes, partic. Hibrinogen, sickle cell has been demonstrated that synthetic peptides beginning with the sequence GPR will bind to fibrinogen. Such peptides include GPR, GPRP and GPRV. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                    Identifying peptides which binds to a specific target - by contacting target with scrambled equilibrium mixt. of many peptide derived from protein by incubation with protease, for detecting potential therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombin; inhibitor; aggregation; platelet; determination; assay; qualitative; quantitative; fibrin.
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                 Random degradation; recombination; scrambling reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 100.0%; Score 25; DB 2; L Local Similarity 100.0%; Pred. No. 1.4e+06; nes 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW09861 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 54; 97pp; English
                                                                                                                                                     93WO-US008231.
                                                                                                                                                                                  92US-00932200
                                                                                                                                                                                                                                                      Hopfinger AJ;
                                                                                                                                                                                                                      (RECE-) RECEPTOR LAB INC
                                                                                                                                                                                                                                                                                      WPI; 1994-083103/10.
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                                                                                                                                                                                      21-AUG-1992;
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                                                                                                                                                     39-AUG-1993;
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                                                                                                                                                                                                                                                      Venton DL,
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                                                   Synthetic.
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Gaps

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100.0%; Score 25; DB 2; Length 4; 100.0%; Pred. No. 1.40+06; iive 0; Mismatches 0; Indels

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AAW25198 and AAW25199 are peptides containing a GPRP sequence. The peptides are capable of binding to cell adhesion molecules and are used in aqueous irrigation solutions for use during and after endoscopic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPRP; glycine; proline; arginine; proline; bladder irrigation; cell adhesion molecule; binding; tumour removal; endoscopic operation; transurethral resection; cancer; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endoscopic irrigation solns. - contg. peptide(s) that bind to cell adhesion molecules.
                                                                                                                                                                                                                                                                                                                                                                                       GPRP-peptide capable of binding cell adhesion molecules.
                                                                                                                                                                                  AAW25198 standard; peptide; 4 AA:
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                                                                                                                                                                                                                                                                                                                          05-JAN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-133793/13.
1 GPRP 4
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GPRP 1 GPRP

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tripoptide, GIV-Pro-Arg is also claimed. This tripoptides sequence tripoptide, GIV-Pro-Arg is also claimed. This tripoptide sequence corresponds to the first 3 amino acids of the alpha-chain exposed by the thrombin catalysed release of the fibrinopeptide A in all vetebrate species. In the present peptide, the addition of a proline residue at postition 4 increases the affinity of the peptide for fibrinogen almost tenfold. These synthetic fibrinogen binding peptides are immobilised on a novel polysaccharide support (e.g. Sephadex), to which they are coupled through a spacer or linker moiety. This linker moiety comprises a chain of greater then 7 atoms. The solid support is useful for the recovery and isolation of fibrinogen from material such as plasma, plasma fractions and fibrinogen by recombinant DNA techniques. The process is superior to other known affinity isolation procedures in that only mild elution buffers are required to recover the bound fibrinogen.
                                                                                                                                                                                                                       ..
0
operations. Preferred irrigation solutions are electrolyte-free and contain I microg/ml to 100 mg/ml of one or more oligopeptides containing the amino acid sequences: RGD, LDV, DDA, DGEA, GPRP, VTL, YIGSR, KOAGDV and/or REDV (given in one letter amino acid code). The solutions are especially used for irrigating the bladder during and after tumour removal by transurethral resection. The peptides protect against recurrence of tumours.
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recovery of fibrinogen using polysaccharide solid support coupled to fibrinogen-binding peptide - requires only mild elution buffers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibrinogen binding peptide; fibrinopeptide A; fibrinogen isolation.
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0
                                                                                                                                                                                    Length 4;
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                                                                                                                                                                                 Score 25; DB 2; I
Pred. No. 1.4e+06;
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic fibrinogen binding peptide 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goss N;
                                                                                                                                                                                                                                                                                                                                                                                 AAW34568 standard; peptide; 4 AA.
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                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative 0
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Matches 4, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-385298/35
                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                       1 GPRP 4
                                                                                                                                                Sequence 4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW34568;
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                                                                                                                                                                                                                                                                                                                                               RESULT 7
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This sequence represents a targeting ligand directed to the GPIIDIIIA

receptor. The invention relates to a contrast agent for diagnostic

imaging or a target composition which comprises: (1) a lipid, protein or

polymer and (ii) a gas, in combination with (iii) a targeting ligand

(TI). TI targets cells or receptors selected from myocardial,

receptor. Also claimed are a composition comprising vesicles containing

(I) - (iii) and an aqueous carrier; a targeted vesicle composition

(I) - (iii) and an aqueous carrier; a targeted vesicle composition

(I) - (iii) and an aqueous carrier; a targeted vesicle composition

(I) - (iii) and a bloactive agent; and a method for providing an tissues or receptors; a formulation for therapeutic or diagnostic use

comprising (i) - (iii) and a bloactive agent; and a method for providing an internal region of a patient, or for diagnosing the presence

of diseased tissue, comprising: (a) administration of a composition as above; and (b) scanning the patient using ultrasound to obtain a visible useful for imaging or diagnosing the presence of diseased tissue,

comprising and addinosing the presence of diseased tissue,

comprising and cardiovascular regions. In particular the ligand targets regions of arrentosclerosis. Stabilised vesicles are particularly useful for perfusion imaging. The vesicles may also be used to deliver

cuttine agents to an intended target such as tissue or a receptor, and

ultrasound can then be used to promote rupture of the vesicles and

release a bioactive or diagnostic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contrast agent or targeted compsn. for imaging or treating diseased tissue - comprising lipid, protein or polymer, a gas, and a targeting ligand e.g. a protein, peptide, saccharide or steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                         Pargeting ligand directed to the glycoprotein GPIIb/IIIa receptor.
                                                                                                                                                                              Contrast agent, targeted composition; diagnosis; diseased tissue; glycoprotein GPIIb/IIIa receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 55; 175pp; English
                 AAW45491 standard; peptide; 4 AA
                                                                                                                                                                                                                                                                                                                                                                                           96WO-US009938
                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00497684
                                                                                                    20-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMAR-) IMARX PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-077233/07.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1996;
                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                               Synthetic.
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Matches
AAW45491
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Gaps

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0; Indels

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Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence contained in fibrin-specific targeting compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Markland FS, Bush LR, Swenson S, Flores Sanchez E;
                                                                                                                                                                                                                                        AAW52073 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYSC-), UNIV SOUTHERN CALIFORNIA.
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(first_entry)
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GPRP 4
                                                              1 GPRP 4
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23-SEP-1998
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                                                                                                                                                                                                                                                                                                           AAW52073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombus
                                                                                                                                                                      RESULT 9
AAM$2073
AAM
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New thrombolytic agents - comprise thrombolytic proteinase covalently linked to targetting compound for binding to component of thrombus. Claim 9; Page 63; 79pp; English.

The invention relates to new thrombolytic agents which comprise a thrombolytic proteinase covalently linked to a targeting compound capable of specifically binding to a component of a thrombus. The thrombolytic agents can be used for eliminating thrombi in vivo in, e.g. myocardial infarction, cerebral ischaemia, deep vein thrombosis or pulmonary embolism. A labelled form of the thrombolytic agent can also be used to image thrombi for diagnostic purposes. The thrombolytic agents are specifically targeted to thrombus sites in vivo and have minimal haemorrhagic side effects and side effects related to non- specific may be used in a fibrin-specific targeting compound. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 4 AA;

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             Length 4;
                                0; Indels
            100.0%; Score 25; DB 2; I 100.0%; Pred. No. 1.4e+06;
                                 Mismatches
                                 .
0
                                  Conservative
Query Match
Best Local Similarity
4; Conserv
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AAY41677 standard; peptide; 4 AA. AAY41677; RESULT 10
AAY41677
ID AAY41
XX
AC AAY41
XX
DT 07-DE
XX

07-DEC-1999

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Fibrin polymerisation inhibitor; factor Xa; thrombin; factor VIII; factor X; caequlation factor; blood; photometric; Protein C anticoaqulant pathway; thromboembolic disease; deep venous thrombosis; pulmonary embolism.
                                  109947699-A1
                           Synthetic.
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Fibrin polymerisation inhibitor peptide.

23-SEP-1999.

99WO-EP001599, 11-MAR-1999; 98EP-00105043. .9-MAR-1998;

(CHRO-) CHROMOGENIX AB

Hall CMY; Rosen BS,

4PI; 1999-571846/48.

New assays for determination of activity of components in the Protein C anticoagulant pathway, used for the study of diseases such as deep venous thrombosis and pulmonary embolism.

Claim 27; Page 50; 67pp; English

Assays have been developed for the determination of activity of components in the Protein C anticoagulant pathway using additional metal in the protein C anticoagulant pathway using additional metal in the protein C anticoagulant pathway of the assays. An in vitro photometric method for qualitative screening and quantitative determination of the functional activity of components of the Protein C anticoagulant pathway of the protein C anticoagulant activity of the enzyme is related to the protein C anticoagulant activity, in a blood sample of a human comprising coagulation factors and the exogenous substrate after at least partial activation of coagulation through the intrinsic, extrinsic, or common pathway and triggering coagulation by: (1) adding calcium ions; and (2) comparing the conversion rate with the conversion rate of a normal human blood sample determined in the same way, characterized by and comparing the conversion rate with the same way, characterized by cadding further metal (s) ions selected from divalent metal ions and conversion to the sample. The method can be used for the global screening for defects in the Protein C activity in a blood sample, for determination of Free Protein S activity in a blood sample, for determination of Protein C activity in a blood sample, and diseases such as deep venous thrombosis and/or pulmonary embolism. The present sequence repersones a fibrin polymerisation inhibitor for use in a method described in the present invention

Sequence 4 AA;

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Gaps
                               0
          Length 4;
                             0; Indels
       100.0%; Score 25; DB 2; I
100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
                                Conservative
Query Match
Best Local Similarity
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AAY31032 standard; peptide; 4 AA. AAY31032; RESULT 11
AAY31032
ID AAY3
XX
AC AP
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21-OCT-1999

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21-MAY-1992;
11-JUL-1994;
21-OCT-1999
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Matches
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                                                                                                                                                                                                                                                                                                                                           This invention describes a novel aqueous suspension of monodisperse particles on non-crosslinked, non-denatured albumin (50-5000 mm) which is stable against dissolving upon dilution with an alcohol-free aqueous medium. The method involves (a) forming an aqueous solution containing albumin and hemoglobin and (b) treating the aqueous solution with an alcohol to cause the solution to become turbid. The particles are useful as agents for in vivo administration, either of their own administration or as a vehicle for other therapeutic or diagnostic agents. The method permits the formation of albumin and hemoglobin particles in the nanometer and micrometer size range, in a form closer to their natural form than the forms of the prior art. The particles therefore constitute a more closely controlled agent for in vivo administration, with greater ease of clearance from the body after their period of usefulness.

AN30952-X31135 represent peptides used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell differentiation, cell proliferation, cell maintenance, estoderm-like cell; embryonic stem cell; plutipotent cell; embryonic stem cell; plutipotent cell; embryonic stem cell; plutipotent cell; gene therapy, cell therapy, tissue transplant; organ transplant; cerotransplant; allotransplant; concomitant transplantation, transgenic animal.
                                                                                                                                                                                                                                                                                                 Non-crosslinked protein particles for therapeutic and diagnostic use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                      Non-crosslinked protein particle; diagnostic; therapy; monodisperse; albumin; haemoglobin; nanometer; micrometer; clearance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell differentiation, proliferation and maintenance factor peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 25; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
Non-crosslinked protein particle peptide 81.
                                                                                                                                                                                                                                                                                                                       Example 22; Col 83-84; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY32378 standard; peptide; 4 AA.
                                                                                                                                                           91US-00641720.
92US-00959560.
93US-00069831.
94US-00212546.
                                                                                                                                    96US-00747137
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                                                                                                                                                                                                                       (HEMO-) HEMOSPHERE INC.
                                                                                                                                                                                                                                                                        WPI; 1999-508153/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4 AA;
                                                                                                                                                         15-JAN-1991;
13-OCT-1992;
01-JUN-1993;
                                                                                                                                   12-NOV-1996;
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                                                                                                                                                                                              14-MAR-1994;
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                                                                                  JS5945033-A
                                                                                                           31-AUG-1999
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This sequence represents a peptide that can form the low mol.wt.

component of a novel biologically active factor that is capable of
influencing the differentiation, proliferation and/or maintenance of
pulripotent cells. The factor consists of a low mol.wt. component

component cells. The factor consists of a low mol.wt. component

collar diy-pro-OH-Pro. a peptide given in AAV3378-82, or a protesse

digested (including collagenase digested) collagen fragment, and a high

mol.wt component such as fibromectin. The biologically active factor is

consisted from conditioned media of hepatic or hepatoma cells or cell

lines or extraembryonic endodermal cells or cell lines. The factor is

capable of causing the transition of pluripotent cells (e.g. embryonic

clls having different properties, more specifically primitive ectoderm-

cells having different properties, more specifically primitive ectoderm-

cells having different properties, more specifically primitive ectoderm-

cells colliferation of these cells in vitro. It also allows the

solation and maintenance of EDE cells derived from in vitro and in vivo

primitive ectoderm. These cells can be used in allo, concomitant- or

replacement, and gene therapy. They can also be used for producing

chimeric or transgenic animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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GPIIb/IIIa receptor, cyclic peptide ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                   New isolated biologically active factor capable of influencing differentiation, proliferation or maintenance of pluripotent cells.
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                                                                                                                                                                                                                                                 Rathjen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 122; 189pp; English
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                                                                  98AU-00002912
98AU-00006097
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94US-00273274.
99WO-AU000265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                 Settess MD, Rathjen PD,
                                                                                                                                                                          (BRES-) BRESAGEN LID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4 AA;
                                                                  09-APR-1998;
23-SEP-1998;
   09-APR-1999;
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                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
                                                                                                              present invention
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bioavailability.
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                                                                                                                                   Sequence 4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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Matches
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AAB98927
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                                                                                                                             This sequence represents the fibrin polymerisation site. The invention relates to a complex (A) for thrombus imaging comprises technetium-99m (TC-99m) completed with a reagent comprising a peptide (P) with 4 to 100 amino acids sequence and a TC-99m binding moiety covalently bound to (P). (P) is selected from a linear peptide ligand for a GPID/IIIa receptor not comprising the amino acid sequence (arginine-glycine-aspartate), a peptide ligand for a polymerisation site of fibrin, and a cyclic peptide ligand for the GPID/IIIa receptor. The thrombus imaging reagents provided by the present invention can be used for visualising thrombi in a mammalian body when TC-99m is labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ultrasound method, useful for diagnosis of e.g. thrombi or carcinomas, uses different types of energy for priming and interrogating the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an ultrasound method comprising: (i) administering a targeted vesicle composition (A); and (ii) scanning the subject by exposure to a first type of ultrasound energy and then
                                                                           comprises technetium-99m complexed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Targeting ligand peptide; imaging; ultrasound; vesicle; tumour; myocardial; endothelial; epithelial; glycoprotein GPIIDIIIa receptor; detection; thrombus; integrin; malignancy; inflammation; lesion; atherosclerotic plaque; carcinoma.
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                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 3; Length 4; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                         A complex used for thrombus imaging comprises with a peptide ligand for GPIIb/IIIa receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 68; 211pp; English
                                                                                                           Claim 7; Col 31-32; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                    AAB20589 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Targeting ligand peptide #5.
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Best Local Similarity 100.00
A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-2000 (first entry)
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          (DIAT-) DIATIDE INC.
                                                    WPI; 2000-021733/02
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                                                                                                                                                                                                                                                        Sequence 4 AA;
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                              Dean RT,
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                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
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interrogating with a second type of ultrasound energy. (A) consists of a vesicle comprising a lipid, protein or polymer, encapsulating a gas, in combination with a targeting ligand. The method is used to detect: (I) a thrombus (particularly old or echogenic); (II) a low concentration of vesicles; or (III) vesicles targeted to endothelial tissue, particularly those containing integrins associated with malignancy or inflammation in early or small lesions, e.g. atherosclerotic plaque or ovarian, encropubbles and reduces background noise. The method increases the signal from microbubbles and reduces background noise. The present sequence represents a targeting ligand peptide which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with an acylated N-methyl-alpha-aminoisobutyryl (NMeAib) molety as the amino protecting group. These can be used in chemical synthesis and in drug delivery. They can be used as produgs which have improved blostability or bloavailability. The present sequence is a peptide described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 3; Length 4; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acylated amino protecting method fibrinogen peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB98927 standard; peptide; 4 AA
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This invention relates to a novel targeted compound having a combination of hydrophobic compound, hydrophilic polymer and targeting ligand. The invention also compities a target vesicle composition comprising lipid, protein or polymer gas filled vesicles in an aqueous carrier, a method for imaging a thrombus in a region of a patient involving administering to the patient a target vehicle composition and scanning the region (preferably cardiac region) with diagnostic imaging (preferably diagnostic ultrasound) and a method for lysing a thrombus in a blood on internal region of a patient which can be used to obtain a visible image of a region (preferably arteriosclerosis, atherosclerotic plaque, infarcted myocardium or a cancer cell) and a method for diagnosing the presence of disease tissue in a patient involving administering a target vehicle composition and scanning the patient using ultrasound to obtain a visible image of the region. The method of the invention may be used for imaging a thrombus in a region of a patient, lysing a thrombus in a blood vessel, diagnosing the presence of diseased tissue in a patient and for the therapeutic delivery in vivo of a placetive agent. The compounds of the invention are easily synthesised and have diagnostic efficacy, and mathod improved targeting a franction over the threatent of the invention are easily synthesised and have diagnostic efficacy over property and a patient and for the method by the presence of diseased tissue or a patient and for the method property argeting efficacy over property argeting a prior of the method of the invention are easily synthesised and have diagnostic of the the the property argeting efficacy over property argeting a parcent of the presence of the property argeting efficacy over property argeting a parcent of the property argeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New targeted compound useful in target vesicle composition for imaging a thrombus in a region of a patient has a combination of hydrophobic compound, hydrophilic polymer and targeting ligand.
                                                                                                                                                                                                                                                                        Target vesicle; diagnostic imaging; thrombus; cancer; arteriosclerosis; atherosclerotic plaque; infarcted myocardium; glycoprotein GPIIbIIIa receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  art methods. The present sequence represents a targeting ligand to the glycoprotein GPIIbIIIa receptor used in the method of the invention
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                                                                                                                                                                                                                              Glycoprotein GpIlbIIIa receptor targeting ligand #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsunaga TO, Schumann PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 65; 206pp; English.
                                                         ABG30381 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMAR-) IMARX THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2001; 2001WO-US032308.
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                                                                                                                                                                     (first entry)
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                                                                                                                                                                     07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                            ABG30381;
RESULT 16
ABG30381
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comprising several oligopeptide units and including recognition sites for peptide cleavage. The products of the invention have cytostatic and antibacterial activity, inhibit tumour cell adhesion and can be used to prepare vaccines. The constructs are used for recombinant production of peptides or their mixtures for use as pharmaceuticals, e.g. a mixture of peptides used, in a rines solution, to reduce the high rate of relapse in superficial bladder carcinoma after transurethral resection or as antimicrobial peptides for control of antibiotic-resistant bacteria in human or veterinary medicine. The constructs allow the possible concentration and reduced cost. This sequence represents an oligopeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA construct encoding polypeptide that includes cleavage sites, useful for preparation of pharmaceutical peptides or their mixtures.
                                                                                                               cytostatic; antibacterial; tumour cell adhesion inhibitor; vaccine; bladder carcinoma; transurethral resection; antimicrobial; human medicine; veterinary medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ultrasound method; targeted vesicle composition; targeting ligand;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 6; Length 4; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Volker L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                construct
                                                                                                                                                                                                                                                                                                                                                                        Sommermeyer K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes a novel DNA
ABG74561 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU63154 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 3; 12pp; German
                                                                                                                                                                                                                                                                                                                                           (FREP ) FRESENIUS KABI DEUT GMBH
                                                                                                                                                                                                                                                                                                             14-MAY-2001; 2001DE-01023348.
                                                                                                                                                                                                                                                                                14-MAY-2001; 2001DE-01023348
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                                                            (first entry)
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                                                                                           Oligopeptide fragment #2.
                                                                                                                                                                                                                                                                                                                                                                        Eichner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-168758/17.
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                                                                                                                                                                                                                   DE10123348-A1.
                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                  21-NOV-2002.
                                                            24-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                          Dormann D,
                                ABG74561;
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Gaps . 0

GPRP

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Length 4;

antirheumatic; antiinflammatory; antiarthritic; peptide therapy; proinflammatory; tetrapeptide; inflammation; synovial joint inflammation; rheumatoid arthritis; fibrinogen A alpha chain; fibrin polymerisation;

Fibrin polymerisation inhibiting peptide seq id 2.

(first entry

15-JAN-2004

ADD32227;

ADD32227 standard; peptide; 4 AA.

ADD32227

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Ultrasound diagnosis, by administering targeted vesicle composition with vesicles encapsulating gas, in combination with targeting ligand, to a patient, and scanning patient by dual frequency ultrasound insonation.
ultrasound scanning, dual frequency ultrasound insonation, micelle, liposome, phospholipid, ultrasound energy, vesicle oscillation, reflected ultrasound signal, ultrasound diagnosis, echogenic thrombus, endothelial tissue, epithelial cell, tumour cell, myocardial cell, integrin, malignancy, inflammation, heart, diseased tissue, imaging, gastrointestinal region, lymphatic system.
                                                                                                                                                                                                                (BRIM ) BRISTOL-MYERS SQUIBB MEDICAL IMAGING INC.
                                                                                                                                                                                                                                                                                                                   Disclosure; Col 49; 96pp; English
                                                                                                                                                            96US-00640464.
96US-00660032.
98US-0073913P.
98US-00218660.
                                                                                                                                 99US-00243640.
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                                                                                                                                                                                                                                                        WPI; 2003-531036/50.
                                                                                                                                                                                                                                    Unger EC, Wu Y;
                                                                                                                                                                        06-JUN-1996;
06-FEB-1998;
22-DEC-1998;
                                                                                                                                 03-FEB-1999;
                                                                                        US6521211-B1
                                                                                                                                                    07-JUN-1995
                                                                                                                                                              01-MAY-1996
                                                                                                             18-FEB-2003
                                                                      Synthetic.
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The present invention relates to a novel ultrasound method which involves administering to a patient a targeted vesicle composition which comprises vesicles encapsulating a gas, in combination with a targeting ligand, and scanning the patient using dual frequency ultrasound insonation. The vesicles themselves comprise a lipid, protein or polymer, and are phospholipid selected from diceleles. The vesicles may comprise a comprise a lipid, protein or polymer, and are phospholipid selected from dicelephonophatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylethanolamine, of succinyldicleoylphosphatidylethanolamine, 1-hexadecyl-2.

The succinyldicleoylphosphatidylethanolamine and phosphatidylethanolamine, of succinyldicleoylphosphatidylethanolamine, 1-hexadecyl-2.

The succinyldicleoylphosphatidylethanolamine in the succinyldicleoylphosphatidylethanolamine, of succinyldicleoylphosphatidylethanolamine, of second phosphatidylethanolamine, new second insonation frequency to cause the vesicle is oscillating, exposing the patient to a second ultrasound energy having a second insonation of frequency that is different from the first insonation frequency, and detecting the reflected ultrasound signal. The method is useful for detecting the reflected ultrasound signal. The method is useful for thrombus or enhancement of thrombus (e.g. old or echogenine associated with malignancy or cargeted to epithelial calls, tumour cells, myocardial cells, and endothelial tissue including integrins associated with malignancy or enforce of diseased tissue in a patient, and for detecting one or more regions of a patient, such as for providing images of the heart, or ensure the presence or regions of a patient, such as sor providing images of the heart, or ensure the present of ensure the present or more the ensure the present of the ensure the present of ensure the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestinal region or lymphatic systems. ABU63151-ABU63172 represent targeting ligands that may be used in the method of the present invention
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synovial or fibroblast cells comprising exposing the cells to a specific tetrapoptide (GPRP) peptide (I). (I) is used for inducing proinflammatory effects in synovial or fibroblast cells. An analogue of (I) is used for treating or preventing inflammation of a synovial joint or rheumatoid arthritis in a subject. (I) is used to identify a receptor for (I) comprising exposing several fibroblastic cells or synovial cells to (I). (I) can identify, isolate and clone the cell receptor to which it binds. This is the amino acid sequence of a fibrin polymerisation inhibiting peptide derived from the human fibrinogen A alpha chain.

The invention describes a method of inducing proinflammatory effects in

Claim 1; SEQ ID NO 2; 16pp; English.

Inducing proinflammatory effects in human synovial or fibroblast cells comprises using a specific tetrapeptide which can also identify a receptor to the tetrapeptide.

IPI; 2003-829401/77

(SMIT/) SMITH T H.

Smith TH;

17-AUG-2001; 2001US-00931009 17-AUG-2001; 2001US-00931009

US2003109431-A1

12-JUN-2003

Homo sapiens

Synthetic

human.

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RESULT 20
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                                                                                                            Length 4;
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                                                                                                       100.0%; Score 25; DB 7; L
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
                                                                                                                                   Conservative
                                                                                                          Query Match
Best Local Similarity
                                                                                  Sequence 4 AA;
                                                                                                                                Matches
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4 GPRP 4

RESULT 19

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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                          Sequence 4 AA;
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                                                                                                                                                                                                                                                                                      Synthetic.
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Matches
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AAR15722 standard; protein; 5 AA.
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                          Stuber W, Fickensche K;
                                                                                                                                                                                                                                                                                                                       (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-334142/46.
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Best Local Similarity
Matches 4; Conserv
                Query Match
Best Local Similarity
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Sequence 5 AA;
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                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. Which inhibit agglomeration of fibrin chains but not thrombin.
                                                                                                                                 New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
Arginine-Proline aminoacid derivs. Which inhibit agglomeration of fibrin
chains but not thrombin.
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                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                       Length 5;
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                                                                                                                                                                                                                                                                         0; Indels
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100.0%; Score 25; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0;
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                                       91EP-00107307.
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                                                         90DE-04014655.
                                                                                                                                                                            Claim 5; Page 8; 8pp; German
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                                                                                                Stuber W, Fickensche K;
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                                                                            (BEHW ) BEHRINGWERKE AG
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                                                                                                                 WPI; 1991-334142/46.
                                                                                                                                                                                                                                                                                                                                                                                                                         Anticoagulant (3).
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                                                                                                                                                                                                                                    Sequence 5 AA;
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                                       06-MAY-1991;
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                    13-NOV-1991
  EP456152-A.
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  Length 5;
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                                                         Indels
100.0%; Score 25; DB 2; L
100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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more
Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
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                                                                         The peptides represented in AAR15718-33 are anticoagulants which are effective than previously known chemically similar cpds. They can be for therapeutic and diagnostic purposes
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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                                            Claim 5; Page 8; 8pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chains but not thrombin.
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                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                      Sequence 5 AA;
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                                                                                                                                                                                                                                1 GPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                      AAR15721;
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AAR15726
ID AAR15
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                                                                                                                                                                                                                                                                                       New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                       /label= G-NH2, G-NH(Ethyl), G-NH(Ethyl)2, G-NH(Butyl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 25; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
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/label= W-NH2, W-NH(Methyl)
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           Location/Qualifiers
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                                                                                                                                 91EP-00107307.
                                                                                                                                                                90DE-04014655.
                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 8; 8pp; German.
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           Key
Misc-difference
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Claim 5; Page 8; 8pp; German.
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                              Claim 5; Page 8; 8pp; German.
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Best Local Similarity 100..
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Best Local Similarity
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Similarity 100.0%; Score 25; DB 2; Length 5;
Similarity 100.0%; Pred. No. 1.4e+06;
4; Conservative 0; Mismatches 0; Indels
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                                               Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
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                                                                                                               91EP-00107307,
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                 (first entry)
                                                                                                                                                             Stuber W, Fickensche K;
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                                 Anticoagulant (9)
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                                                                Synthetic.
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  AAR15726;
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AAR15724
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New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
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                                                                                                                                                                                                                                                                                                                                                                                          Length 5;
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AAR15719
ID AAR15719 standard; protein; 5 AA.
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Gaps

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The peptides represented in AAR15718-33 are anticoagulants which are more effective than previously known chemically similar cpds. They can be used for therapeutic and diagnostic purposes
                                                                                                   New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blood coagulation inhibiting peptide.
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                                                                                                                                                                               Claim 5; Page 8; 8pp; German.
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                      Fickensche
                                                              WPI; 1991-334142/46.
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Best Local Similarity
Matches 4; Conserv
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                        Stuber W,
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                                                                                                                                                                                                                                                    /label= S-NH2, S-NH(Isopropyl)
                                                                                                                                                                                                          Location/Qualifiers
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                                                       (first entry)
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                                                                                                                                                                         Synthetic
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                  AAR15719
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The blood coagulation inhibiting peptide conprises L-form amino acids and has fibrin agglutination inhibiting activity. Such peptides (see AAR60327-860335) were synthesisers (Applied Bloosystems Co., 430A) and purified by high pressure liquid chromatography. To 0.2 m of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was added and incubated for I minute at 37 deg Celsius. 0.2 m of thrombin solution was added and the ICSO was determined according to the method of Kawasaki et al. This peptide had an ICSO of 65 micromolar compared with a control peptide of Gly-Pro-Arg which registered an ICSO of 250 micromolar
New blood coagulation inhibiting peptide(s) having fibrin-agglutination inhibitory activity - useful for the treatment and prevention of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 2; Length 5; Pred. No. 1.4e+06;
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100.0%;
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Best Local Similarity
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(BEHW) BEHRINGWERKE

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The blood coagulation inhibiting peptide comprises L-form amino acids and has fibrin agglutination inhibiting activity. Such peptides (see AAR60327 *R60335) were synthesiser (Applied Blosystems Co., 430A) and purified by high pressure liquid chromatography. To 0.2 ml of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was added and incubated for I minute at 37 deg Celsius. 0.2 ml of thrombin solution was added and the IC50 was determined according to the method of Kawasaki et al. This peptide had an IC50 of 65 micromolar compared with a control peptide of Gly-Pro-Arg which registered an IC50 of 250 micromolar
                                                                                                                                                                                                  New blood coagulation inhibiting peptide(s) having fibrin-agglutination inhibitory activity - useful for the treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombin; inhibitor; aggregation; platelet; determination; assay; qualitative; quantitative; fibrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Score 25; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.40+06;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                    SCI & TECHNOLOGY.
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                                                                                                                                                                                                                                                            Claim 1; Page 2; 6pp; Japanese.
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                                                                              93JP-00085678
                                                                                                          92JP-00300380
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                                                                                                                                  OF IND !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombin inhibitor.
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                                                                                                                                    (AGEN ) AGENCY
(NIHA-) NIPPON
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Modified-site
                        JP06179696-A
                                                                               19-MAR-1993;
                                                                                                          13-OCT-1992;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The blood coagulation inhibiting peptide comprises L-form amino acids and has fibrin agglutination inhibiting activity. Such peptides (see AAR60327 4860335) were synthesiser (Applied Blosystems Co., 430A) and purified by high pressure liquid chromatography. To 0.2 ml of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was added and incubated for 1 minute at 37 deg. Celsius. 0.2 ml of thrombin solution was added and the IC50 was determined according to the method of Kawasaki et al. This peptide had an IC50 of 50 micromolar compared with a control peptide of Gly-Pro-Arg which registered an IC50 of 250 micromolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New blood coagulation inhibiting peptide(s) having fibrin-agglutination inhibitory activity - useful for the treatment and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                         AAR60330 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1, Page 2, 6pp; Japanese.
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Similarity 100.0%;
4; Conservative 0;
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  4; Conservative
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(NIHA-) NIPPON
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                                                                                                                                                                                                                                                                 Synthetic
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Best Local S:
Matches 4
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AAR60334
  Matches
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Peptides AAW34568-71 are synthetic fibrinogen binding peptides. A tripeptide, Gly-Pro-Arg is also claimed. This tripeptide sequence corresponds to the first 3 amino acids of the alpha-chain exposed by the thrombin catalysed release of the fibrinopeptide A in all vetebrate species. In peptide AAW34568, the addition of a proline residue at position 4 increases the affinity of the peptide for fibrinogen almost refiold. These synthetic fibrinogen binding peptides are immobilised on a novel polysaccharide support (e.g. Sephadex), to which they are coupled through a spacer or linker moiety. This linker moiety comprises a chain of greater then 7 atoms. The solid support is useful for the recovery and isolation of fibrinogen from material such as plasma, plasma fractions and fibrinogen-containing cell culture media arising from the production of fibrinogen by recombinant DNA techniques. The process is superior to
                                                                                                                                                 In the qualitative or quantitative determn. of thrombin-induced platelet aggregation in the presence of fibrin, interference from fibrin clot formation is suppressed with a fibrin-aggregation inhibitor (e.g. AAM09661-63). The assay may be used to determine the platelet aggregation inhibitory activity of thrombin inhibitors. The peptides inhibit fibrin clot formation at high thrombin concns. without inhibiting platelet
                                    Determn. of thrombin-induced platelet aggregation in presence of fibrin comprises use of fibrin aggregation inhibitor to suppress fibrin clot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recovery of fibrinogen using polysaccharide solid support coupled to fibrinogen-binding peptide - requires only mild elution buffers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibrinogen binding peptide; fibrinopeptide A; fibrinogen isolation.
                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 25; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic fibrinogen binding peptide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW34570 standard; peptide; 5 AA.
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                                                                                                                Claim 5; Col 6; 5pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanellos J, Pham H,
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                                                                             Formation
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                                                                                                                                                                                                                                                                                     Immobilised ligand; inactivation; virus; binding; thrombin; denaturation; affinity; fibrinogen; purification.
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                              Indels
 Length
                                                                                                                                                                                                                                                           Peptide ligand used in purification of fibrinogen.
100.0%; Score 25; DB 2; I 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0;
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                                                                                                                                                                    AAW47188 standard; peptide; 5 AA.
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Best Local Similarity
   Query Match
Best Local Similarity
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                                                           1 GPRP
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                                 Matches
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other known affinity isolation procedures in that only mild elution buffers are required to recover the bound fibrinogen

Sequence 5 AA;

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WPI; 1995-233339/31

/note= "residue can be Lys, polylysine or a spacer"

Misc-difference 5

WO9902565-A2

21-JAN-1999

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Fibrinogen; ligand; fibrin; treatment; prevention; rheology; diabetes; microcirculatory disorder; retinopathy; polymeuropathy; apoplexy; sepsis; hearing loss; sepsis, occlusive arterial disease; kidney function.

Location/Qualifiers

AAW92897 standard; peptide; 5 AA Fibrinogen ligand peptide #1 (first entry) 14-MAY-1999 Synthetic AAW92897 RESULT 38 AAW92897

Using ligand for fibrinogen or fibrin to treat or prevent microcirculatory disorders - and to control blood rheology, e.g. diabetes -related conditions, also adsorber material with bound ligand for the This invention describes the use of a ligand for fibrinogen and/or fibrin for prevenenting microcirculatory disorders and/or for modifying rheology, in mammals. The products of the invention can be specifically used to treat or prevent disorders associated with diabetes, retinopathy, polyneuropathy, apoplaxy, hearing loss, sepsis, occlusive arterial disease and/or impaired kidney function Reducing the amount of fibrinogen and/or fibrin in the blood allevates Fibrinogen, ligand, fibrin, treatment, prevention, rheology, diabetes, microcirculatory disorder, retinopathy, polyneuropathy, apoplexy, sepsis, hearing loss, sepsis, occlusive arterial disease, kidney function. (THER-) THERASORB MEDIZINISCHE SYSTEME GMBH. Tschoepe W; Example 1; Page 15; 23pp; German. AAW92898 standard; peptide; 5 AA. Bieber F, Fibrinogen ligand peptide #2 97DE-01029591 (first entry) Richter W, WPI; 1999-120788/10. disease symptoms Sequence 5 AA; WO9902565-A2 10-JUL-1997; 14-MAY-1999 21-JAN-1999 AAW92898; Koll R,

1 GPRP 4 ð d

. 0 Gaps ö Length 5 0; Indels Score 25; DB 2; I Pred. No. 1.4e+06; 0; Mismatches 0; n Similarity 100.0%; 4; Conservative 0;

Query Match Best Local Similarity Matches 4; Conserv 1 GPRP 4

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07-DEC-2001; 2001WO-AT000387

Location/Qualifiers Key Modified-site WO200248180-A2 20-JUN-2002

12-DEC-2000; 2000AT-00002063

This invention describes the use of a ligand for fibrinogen and/or fibrin for preventing microcirculatory disorders and/or for modifying rheology, in mammals. The products of the invention can be specifically used to treat or prevent disorders satisficated with diabetes, retinopathy, polyneuropathy, apoplexy, hearing loss, sepsis, occlusive arterial disease and/or impaired kidney function Reducing the amount of fibrinogen and/or fibrin in the blood alleviates

disease symptoms

Sequence 5 AA;

Length 5; Indels Score 25; DB 2; Li Pred. No. 1.4e+06; 0; Mismatches 0; 100.0%; Similarity 100.0%; 4; Conservative 0; Query Match Best Local Similarity Matches 4; Conserv

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AA018327 standard; peptide; 5 AA AA018327 AA01832

Fibrinogen based therapeutic peptide #3. (first entry) 11-OCT-2002

Fibrin, fibrinogen; antagonist; inflammation; autoimmune disease; rheumatic disease; organ transplantation; arteriosclerosis; reperfusion trauma; thrombosis; cancer; antiinflammatory; antibacterial; immunosuppressive; antirheumatic; antiarteriosclerotic; vasotropic; thrombolytic; anticosqulant; cytostatic; antipsoriatic.

Unidentified

/note= "linked to between 2 and 30 peptide residues"

Disclosure; Page 14; 23pp; German.

Using ligand for fibrinogen or fibrin to treat or prevent microcirculatory disorders - and to control blood rheology, e.g. diabetes -related conditions, also adsorber material with bound ligand for the

(THER-) THERASORB MEDIZINISCHE SYSTEME GMBH.

97DE-01029591.

10-JUL-1997;

Tschoepe W;

Bieber F,

Richter W,

WPI; 1999-120788/10.

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us-09-931-009a-2.open.rag

combating fibrin-mediated disorders such as inflammation, transplant rejection, arteriosclerosis and reperfusion damage.

Peptides or proteins based on fibrin or fibrinogen sequences, useful for (FIBR-) FIBREX MEDICAL RES & DEV GMBH WPI; 2002-557605/59 WPI; 2002-557605/59. Local Similarity 1 GPRP 4 1 GPRP 4 WO200248180-A2 Sequence 5 AA; Key Modified-site Unidentified 11-0CT-2002 Petzelbauer 20-JUN-2002 Query Match AA018329 Matches δ

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The present invention relates to peptides based on the alpha- and betachain sequences of fibrin/fibrinogen, which are capable of acting as fibrin antagonists. These are used for the therapy of local and generalised inflammation associated with infection, autoimmune reactions, rheumatic disease, immune system dysfunction or genetic disease, for the prevention and treatment of organ transplantation rejection reactions, arteriosclerosis, reperfusion trauma, thrombotic disease and increased fibrin deposition associated with aging, or for the transport of other medicaments to human or animal endothelial cells. They may also be effective against fibrin-mediated tumour growth, collagenosis or psoriasis. The present sequence is a peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match. 100.0%; Score 25; DB 5; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                             Claim 2; Page 36; 41pp; German
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AAR15733
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                                                                                                                                                                                                                                                                     The present invention relates to peptides based on the alpha- and betachain sequences of fibrin/fibrinogen, which are capable of acting as fibrin matgonists. These are used for the therapy of local and generalised inflammation associated with infection, autoimmune reactions, rheumatic disease, immune system dysfunction or genetic disease, for the prevention and treatment of organ transplantation rejection reactions, arteriosclerosis, reperfusion transm. thrombotic disease and increased fibrin deposition associated with aging, or for the transport of other medicaments to human or animal endotherial cells. They may also be effective against fibrin-mediated tumour growth, collagenosis or psoriasis. The present sequence is a peptide of the invention
                                                                                                                                            Peptides or proteins based on fibrin or fibrinogen sequences, useful for combating fibrin-mediated disorders such as inflammation, transplant rejection, arteriosclerosis and reperfusion damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatic disease; organ transplantation; arteriosclerosis; reperfusion trauma; thrombosis; anteriosclerory; antibacterial; immunosuppressive; antirheumatic; antiarteriosclerotic; vasotropic; thrombolytic; anticoagulant; cytostatic; antipsoriatic.
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/note= "linked to between 2 and 30 peptide residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibrin, fibrinogen; antagonist; inflammation; autoimmune disease;
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                                                                                                                                                                                                                                Claim 2; Page 34; 41pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-2000; 2000AT-00002063
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New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= P-NH2, P-NH(Isopropyl)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                           AAR15733 standard; protein; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 8; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91EP-00107307
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stuber W, Fickensche K;
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91EP-00107307,
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                                                                                                                                                                         Stuber W, Fickensche K;
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                                                                                                                                                    (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                              WPI; 1991-334142/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-334142/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anticoagulant (15)
                     Key
Misc-difference
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                          1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                               1 GPRP 4
                                                                                                                                                                                                                                                                                                                            Sequence 6 AA;
                                                                                                          06-MAY-1991;
                                                                                                                               08-MAY-1990;
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                                                                                    13-NOV-1991,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-1991
                                                                EP456152-A.
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  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR15732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                    New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. Which inhibit agglomeration of fibrin chains but not thrombin.
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The peptides represented in AAR15718-33 are anticoagulants which are effective than previously known chemically similar cpds. They can be for therapeutic and diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
            ;
0
                                                                                                                                                                                            Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibrin, anticoagulant; inhibitor; therapeutic; diagnosis.
; Pred. No. 1.4e+06; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 25; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                           /label= P-NH2, P-NH(Isopropyl)
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                         AAR15730 standard; protein; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR15731 standard; protein; 6 AA.
100.08;
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                                                                                                                                                                                                                                                                                                                                                 90DE-04014655.
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                                                                                                                                                  (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Fickensche K;
                                                                                                                                                                                                                                                                                                                                                                     (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-334142/46.
                                                                                                                                                                        Anticoagulant (13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anticoagulant (14)
                                                                                                                                                                                                                                       Key
Misc-difference
                              1 GPRP 4
                                                    GPRP 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6 AA;
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                                                                                                                                                                                                                                                                                                                                                08-MAY-1990;
                                                                                                                                                    24-JAN-1992
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                                                                                                                                                                                                                                                                                                       13-NOV-1991
                                                                                                                                                                                                                                                                                 EP456152-A.
                                                                                                                                                                                                                                                                                                                                                                                          Stuber W,
                                                                                                                                                                                                                   Synthetic.
                                                                                                                              AAR15730;
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AAR15731
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The peptides represented in AAR15718-33 are anticoagulants which are more effective than previously known chemically similar cpds. They can be used for therapeutic and diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
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                                                                      /label= P-NH2, P-NH(Isopropyl)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR15732 standard; protein; 6 AA.
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New blood coagulation inhibiting peptide(s) having fibrin-agglutination inhibitory activity - useful for the treatment and prevention of thrombosis.
                                                                                                                             Blood; fibrin; coagulation; inhibition; thrombin; fibrinogen.
                                                                                                                                                                                                                                                               (AGEN ) AGENCY OF IND SCI & TECHNOLOGY. (NIHA-) NIPPON HAM KK.
                                                                                                      Blood coagulation inhibiting peptide.
                                      AAR60332 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                 WPI; 1994-245692/30.
                                                                                                                                                                        JP06179696-A.
                                                                                                                                                                                                                    19-MAR-1993;
                                                                                                                                                                                                                                          13-OCT-1992;
                                                                                  07-MAR-1995
                                                                                                                                                                                             28-JUN-1994.
                                                                                                                                                  Synthetic.
                                                           AAR60332;
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                RESULT 46
AAR60332
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New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin chains but not thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New anticoagulant penta- and hexa:peptide(s) - are Glycine-Proline-Arginine-Proline aminoacid derivs. which inhibit agglomeration of fibrin
                                                                 The peptides represented in AAR15718-33 are anticoagulants which are effective than previously known chemically similar cpds. They can be for therapeutic and diagnostic purposes
                                                                                                                                                              Gaps
                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                   Fibrin; anticoagulant; inhibitor; therapeutic; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6;
                                                                                                                                                            0; Indels
                                                                                                                                      Length
                                                                                                                                    100.0%; Score 25; DB 2; L
100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
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Similarity 100.0%; Pred. No. 1.4e+06;
4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     /label= P-NH2, P-NH(Isopropyl)
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                           AAR15729 standard; protein; 6 AA.
                                             Claim 5; Page 8; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 8; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90DE-04014655,
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                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arginine-Proline aminoac chains but not thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fickensche K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-334142/46.
                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                              Anticoagulant (12)
                                                                                                                                                                                1 GPRP 4
                                                                                                                                                                                                     GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                              Sequence 6 AA;
                                                                                                                                                                                                                                                                                                       24-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stuber W,
                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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  FFFXSXSSSXS
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92JP-00300380

(first entry)

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The blood coagulation inhibiting peptide conprises L-form amino acids and has fibrin agglutination inhibiting activity. Such peptides (see AAR60327-R60335) were synthesised using a peptide synthesiser (Applied Biosystems Co., 430A) and purified by high pressure liquid chromatography. TO 0.2 ml of fibrinogen solution (2.5 mg/ml), 0.2 ml of test peptide solution was added and incubated for 1 minute at 37 deg. Celsius. 0.2 ml of thrombin solution was added and the ICSO was determined according to the method of Kawasaki et al. This peptide had an ICSO of 70 micromolar compared with a control peptide of Gly-Pro-Arg which registered an ICSO of 250 micromolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fibrin-alpha-chain; Tc-99m thrombus detection; deep venous thrombosis; DVT; pulmonary embolism; PE; cell image; technetium-99m.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 .
0
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                                                                                                                                                                                                                                                                                                                                             n 100.0%; Score 25; DB 2; Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78985 standard; peptide; 6 AA.
Claim 1; Page 2; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= 4Abu
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GPRP 4
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                                                                                                                                                                                                                                                                                               Sequence 6 AA;
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Modified-site
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Gaps

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/note= "The C-terminal has a TC-99m-complexed peptide of formula NH2-Gly-Ala-Gly-Gly-CO-NH- condensed onto it"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Characterizing a target that binds to a ligand, useful in concentrating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method of imaging cells or tissues such as thrombus, particularly deep venous thrombosis and pulmonary embolism comprising using novel radiolabeled fibrin-alpha-chain peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ligand; target; matrix; binding characteristic; isoform; enantiomer; modification; fVIII; factor VIII; vWF; von Willebrand's factor.
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Pred. No. 1.4e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE86867 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lathrop JT;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003089922-A1
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                                                                                                WO200009076-A2
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This sequence represents a ligand which binds fibrinogen. This ligand was identified using the method of the invention for characterizing a target identified using the method of the invention for characterizing a target that binds to a ligand, The method comprises transferring at least a portion of the target one target within the second matrix, where the position of the ligand-support complex to a second matrix, and detecting the target on the second matrix. The support corresponds to the position of the ligand-support complex within the second matrix. It is matrix, and detecting the target on the second matrix. The support conder that binds to a ligand or in determining preferred conditions under which a target or any molecule is transferred to the second matrix. It also provides a means to study the binding characteristics of the target and/or ligand. The method is also useful in separating isoforms and enantiomers from a sample. Detecting target-ligand binding of the invention avoids modification of the target for detection, enables detection avoids modification of the target via its biological, blochemical or chemical activity compared to currently available detection rethingues which have potential drawbacks, namely modification charget-detection systems already exist. Immited number of targets for which detection systems already exist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing a primate neural cell, useful for treating Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primate neural cell; pluripotent primate cell; MEDII; neural disease; Parkinson's disease; Huntington's disease; ysosomal storage disease; multiple sclerosis; memory disorder; behavioural disorder; disease; Alzheimer's disease; macular degeneration; toxicity testing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
or separating target molecules form a sample comprises transferring portion of the target of least one target-ligand-support complex to second matrix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 8; Length 6; ilarity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels
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(BRES-) BRESAGEN LTD.
                                                                                      Example 6; Page 19; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD69979 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2003; 2003WO-US007665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2002; 2002US-0364381P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proline-containing peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-779126/73
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The invention comprises a method for producing a primate neural cell, the method involves culturing a pluripotent primate cell with a MEDII conditioned medium. The method and the primate neural cell of the invention are useful for treating a neural disease, such as: Parkinson's disease, Huntington's disease, lysosomal storage diseases, multiple macular degeneration. The neural disorders, Alzheimer's disease, and macular degeneration. The neural cells are also useful for testing the effect of molecules on neural differentiation or survival, in toxicity functions. The present amino acid sequence represents a proline-containing peptide that may be used in the MEDII conditioned medium in the method of the invention.
Alzheimer's disease, Huntington's disease, or macular degeneration, comprises culturing a pluripotent primate cell with a MEDII conditioned
                                                                                                                                                                                                               Disclosure; SEQ ID NO 1; 36pp; English
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Gaps ; 0 100.0%; Score 25; DB 7; Length 7; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels 0; Indels Conservative Local Similarity les 4; Conserv 1 GPRP 4 Sequence 7 AA; Query Match Best Loc Matches à

4 GPRP 7 a

RESULT 50

AAR69319 standard; peptide; 8 AA. AAR69319;

Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi. (revised)
(first entry) 25-MAR-2003 25-JUN-1995

Scintigraphy, thrombus, thrombi, imaging, specific binding, technetium-99m, radiolabelled, Gp IIb/IIIa receptor ligand.

Synthetic.

/note= "S-acetamidomethyl-Cys" Location/Qualifiers Key Modified-site Modified-site /note= "this residue is joined via the SH group to tris(2 -succinimidoethyl)amine (TSEA) to form one of three such peptides connected to the amine; i.e. forming a product of formula (peptide)3-TSEA"

'note= "S-acetamidomethyl-Cys"

Modified-site

WO9323085-A1

25-NOV-1993

21-MAY-1993;

92US-00886752 21-MAY-1992;

(DIAT-) DIATECH INC

Lister-James J;

Dean RT,

WPI; 1993-386229/48.

Reagent for scintigraphic imaging of thrombi with 99m technetium -comprises synthetic peptide which binds to thrombus covalently coupled to

metal binding gp., rapidly cleared from blood and tissue. Claim 19; Page 42; 61pp; English.

The invention relates to reagents for scintigraphic imaging of a thrombus in-vivo, comprising (A) a specific binding compound capable of binding to at least one component of a thrombus, covalently linked to (B) a technetium-99m-binding moiety. Specific peptides constituting the reagents are claimed as new. The present peptide is one such peptide, in which the Cys(Ann) Gly-Cys(Asm) moiety is the 99m-Tc binding moiety and the residue constitutes the thrombus- binding component. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 8 AA;

Gaps ; 0 100.0%; Score 25; DB 2; Length 8; Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Indels 0; Indels Best_Local Similarity Matches 4; Conserv Query Match

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1 GPRP 4

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7, 2004, 18:58:18 Search completed: September Job time : 127 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

7, 2004, 19:25:22 ; Search time 122 Seconds (without alignments) 10.330 Million cell updates/sec September Run on:

US-09-931-009A-2 25 1 GPRP 4 Title: . Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1298764 seqs, 315065143 residues Searched:

7583 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 4

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65 summaries

/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.ppg.*
/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.ppg.*
/ cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppg.*
/ cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppg.*
/ cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppg.*
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/ cgn2_6/ptodata/2/pubpaa/US60A_PUBCOMB.ppg.* Published Applications AA:*

(cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep::/cgn2_6/ptodata/2/pubpaa/PUS06_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep::/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:://cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:://cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:://cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:://cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 16, Appl	Sequence 2, Appli	Sequence 6, Appli	25	Sequence 25, Appl	Sequence 101, App	Sequence 34, Appl	Sequence 115, App	Sequence 8, Appli	Sequence 24, Appl	Sequence 30, Appl	Sequence 26, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 4, Appli
		OI.	US-09-779-054-16	US-09-931-009A-2	US-10-046-801-6	US-10-016-569A-25	US-10-308-644-25	US-10-243-613-101	US-10-275-427A-34	US-10-211-088-115	US-09-040-518-8	US-09-804-733A-24	US-09-765-614B-30	US-09-925-715-26	US-09-807-742-3	US-10-619-520-3	US-10-619-520-4
		DB	9	10	14	15	12	12	12	14	σ	σ	σ	a	11	12	12
		Match Length DB	4	4	4	4	4	m	4	4	4	4	4	4	4	4	4
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ALIGNMENTS

Sequence 16, Application US/09779054

Patent No. US200201201201

Patent No. US2002012012012

APPLICANT: Lu, Xinjie

APPLICANT: Lu, Xinjie

APPLICANT: Kakkar, Vijay

TITLE OF INVENTION: USE OF DENDROASPIN AS A SCAFFOLD FOR NON-DENDROASPIN DOMAINS
FILE REFERENCE: A-70312/TAL/AMS

CURRENT APPLICATION NUMBER: US/09/779,054

CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: GB 0002625.2

PRIOR APPLICATION NUMBER: GB 0002625.2

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin version 3.0 RESULT 1 US-09-779-054-16 SEQ ID NO 16 LENGTH: 4 TYPE: PRT

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Secure 25, Application US/10308644

Publication No. US20030229017A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wu, Shih-Kwang

APPLICANT: Chang, Ting-Gung

APPLICANT: Shih, Kea-Shyang

TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing

FILE REFERENCE: P1379

CURRENT APPLICATION NUMBER: US/10/308,644

CURRENT PILING DATE: 2002-12-03

NUMBER OF SEQ ID NOS: 29

SOFTWARE PREDENT NOS: 29
                                                         Sequence 25, Application US/10016569A
Sequence 25, Application US/10016569A
Sequence 25, Application US/10016569A
Sequence 25, Application US/20030229013A1
GENERAL INFORMATION:
APPLICANT: Treeng, Chin._Lu
APPLICANT: Cheng, Ting-Gung
APPLICANT: Cheng, Li-Jung
APPLICANT: Shih, Kea-Shyang
APPLICANT: Shih, Kea-Shyang
APPLICANT: Conjugates Synthesized Thereby and Targeted Liposomes Containing
TITLE OF INVENTION: the Same
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Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/016,569A CURRENT FILING DATE: 2001-12-07 NUMBER OF SEQ ID NOS: 29 SOFWARE: Patentin version 3.2 SEQ ID NO 25
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US-10-308-644-25
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TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027Alel Sequenc
US-10-046-801-6
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                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
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US-10-046-801-6
Sequence 6, Application US/10046801
Publication No. US20030054027A1
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.;
TITLE OF INVENTION: Charged Lipids and Uses For The Same FILE REFERENCE: UNGR1592
CURRENT APPLICATION NUMBER: US/09/540,448
PRIOR FILING DATE: 2002-05-13
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 1997-09-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: 1997-09-08
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4;
                                                                                                              Length 4;
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Publication No. US20030109431A1
GENERAL INFORMATION:
TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE
FILE REPERENCE: US 1257/01 (VA)
CURRENT APPLICATION UNMBER: US/09/931,009A
UNMBER OF SEQ ID NOS: 2
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Similarity 100.0%; Pred. No. 1.2e+06;
4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0;
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: thrombin-binding sequence
US-09-779-054-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 4
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US-09-804-733A-24

US-09-804-733A-24

Sequence 24, Application US/09804733A

Sequence 24, Application US/09804733A

Sequence 24, Application US/09804733A

Setent No. US20020059656A1

GENERAL INFORMATION:

SEPLICANT: Monsanto Company

TITLE OF INVENTION: RECOMBINAT PROTEINS CONTAINING REPEATING UNITS

FILE REFERENCE: MTG6614.2

CURRENT APPLICATION NUMBER: US/09/804,733A

CURRENT APPLICATION NUMBER: US 60/188,990

PRIOR PILING DATE: 2000-03-13

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn version 3.0

SEQ ID NO 24

LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-040-518-8

US-09-040-518-8

Sequence 8, Application US/09040518

Patent No. US2001004225541

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: PRODUCTION OF BIOFILAMENTS IN TRANSGENIC

TITLE OF INVENTION: ANIMALS

FILE REFERENCE: 06632/011001

CURRENT APPLICATION WUMBER: US/09/040,518

CURRENT PILING DATE: 1998-03-17

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 8

TANDER OF SECON WINDOWS OF SEQ ID NOS: 32
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76.0%; Score 19; DB 14; 1
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0;
        FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-12-13
NUMBER: OF SEQ ID NOS: 366
SECTIANARE: PATENTIN VERSION 3.1
SEQ ID NO 115
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORCANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Binding domain
US-10-211-088-115
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 3; Conservative
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Publication No. US20030104479A1
GENERAL INFORMATION:
APPLICANT: Bright, Gary R.
APPLICANT: Prenkumar, D. David
APPLICANT: Chen, Yih-Tai
APPLICANT: Chen, Yih-Tai
TITLE OF INVENTION: No. US20030104479A1e1 Fusion Proteins And Assays For Molecular Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nash et al.

TITLE OF INVENTION: Molecules that Modulate Ubiquitin-Dependent Proteolysis and
TITLE OF INVENTION: Methods for Identifying Same
FITLE OF INVENTION: Methods for Identifying Same
FITLE OF INVENTION: Methods for Identifying Same
FILE REPERENCE: MTS1-PO1-011

CURRENT APPLICATION NUMBER: US/10/275,427A

CURRENT APPLICATION NUMBER: PCT/CA01/00632

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 34

LENGTH: 4
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APPLICANT: Chen, Emily I.

APPLICANT: Kridel, Steven J.

ITLE OF INVENTION: Selective Substrates for Matrix

ITLE OF INVENTION: Metalloproteinases

TITLE OF INVENTION: Metalloproteinases

FILE REFERENCE: P.L/S 43.2

CURRENT APPLICATION NUMBER: US/10/243,613

PRIOR APPLICATION NUMBER: US 09/953,592

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 129

SOFTWARE: RastSEQ for Windows Version 4.0

SEQ ID NO 101

LENGTH: 3
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76.0%; Score 19; DB 12;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 1.
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Sequence 34, Application US/10275427A
Publication No. US20040072319A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: CDP Peptide
                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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LOCATION: (4)...(4
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Query Match 72.0%; Score 18; DB 12; I
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0;
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LOCATION: (1)...(4)
OTHER INFORMATION: X is any amino acid
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; OTHER INFORMATION: Synthesized Peptide US-10-619-520-3
Best Local Similarity 100.0%; P
Matches 3; Conservative 0;
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Best Local Similarity 75.0%;
Matches 3; Conservative
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LENGIH: 4
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US-09-925-715-26
Sequence 26, Application US/09925715
Sequence 26, Application US/09925715
Sequence 26, Application US/09925715
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REPERENCE: REF/Klaveness/206
CURRENT APPLICATION NUMBER: US/09/925,715
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 26
LENGTH: 4
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72.0%; Score 18; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                       0; Indels
                                                                                                                                                              72.0%; Score 18; DB 9; Length 4; 100.0%; Pred. No. 1.2e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or relating to
                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Application US/09765614B
Patent No. US20020102215A1
GENERAL INFORMATION:
APPLICANT: NYCOMED Imaging AS
TITLE OF INVENTION: Improvements in or relatin;
TITLE OF INVENTION: adaptostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT PAPLICATION NUMBER: US/09/765,614B
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:Thrombus OTHER INFORMATION: binding peptide US-09-765-6148-30
    TYPE: PRT
CRGANISM: Artificial Sequence
PRATURE:
NAME/KEY: VARIANT
COCATION: (1)...(4)
COTHER INFORMATION: Trypsin cleavage site
US-09-804-733A-24
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 3; Conservative
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US-09-765-614B-30
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Squence 3, Application US/10619520

Requence 3, Application US/10619520

Requence 3, Application US/20040057957A1

GENERAL INFORMATION:

APPLICANT: Richer, W.

APPLICANT: Bieber, Franz

APPLICANT: Bieber, Franz

APPLICANT: Tachoppe, W.

TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIFFILE REPERENCE: Attorney Docket No. US20040057957A1 1328/2

CURRENT APPLICATION NUMBER: US/10/619,520

CURRENT PILING DATE: 2003-07-14

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                 Sequence 3, Application US/09807742;
Sequence 3, Application US/09807742;
Publication No. US20030204864A1
GENERAL INFORMATION:
APPLICANT: DANIELL, HENRY
TITLE OF INVENTION: PRODUCTION OF PHARMACEUTICAL PROTEINS IN TRANSGENIC
TITLE OF INVENTION: PLASTIDS
FILE REPRENCE: 1465-PCT-US-00
CURRENT APPLICATION NUMBER: US/09/807,742
CURRENT PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 4
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                        Gaps
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                        Indels
Pred. No. 1.2e+06;
Mismatches 0;
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CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: sptrembl/Q9UCG8/Q9UCG8
US-10-028-075B-151
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US-10-028-075B-151
US-10-028-075B-151
Sequence 151, Application US/10028075B
Publication No. US20030113733A1
GENERAL INFORMATION:
APPLICANT: Khan, Nisar A.
APPLICANT: Benner, Robert
TILE OF INVENTION: Gene regulator
FILE REFERENCE: 2183-5223US
CURRENT APPLICATION NUMBER: US/10/028,075B
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EP 01203748.7
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 175
SEQ ID NO 151
LENGTH 4
TWOST THAT
    Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
3; Conservative
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| Sequence 5, Application US/10619520 |
| Sequence 5, Application US/10619520 |
| Publication No. US20040057957A1 |
| Publication No. US20040057957A1 |
| APPLICANT: Robert, Koll |
| APPLICANT: Richer, W. |
| APPLICANT: Richer, Fanz |
| APPLICANT: Tschoppe, W. |
| TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DI FILE REPERRINCE: Attorney Docket No. US20040057957A1 1328/2 |
| CURRENT APPLICATION NUMBER: US/10/619,520 |
| CURRENT FILING DATE: 2003-07-14 |
| WUMBER OF SEQ ID NOS: 8 |
| SOFTWARE: Patentin version 3.0 |
| SEQ ID NO 5 |
| TYPE: PRT |
| TYPE: PRT |
| TYPE: PRT |
| OGGANISM: Artificial Sequence |
| OGGANISM: ARTIFICANT |
| OGGANISM: Artificial Sequence |
| OGGANISM: ARTIFICATION SECONTICATION 
                                                                                                                                                                                                                                                                                Sequence 4. Application US/10619520
Publication No. US20040057957A1
Publication No. US20040057957A1
Publication No. US20040057957A1
APPLICANT: Robert, Koll
APPLICANT: Richter, W.
APPLICANT: Baber, Franz
APPLICANT: Ask of Second Control of Second Contro
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0;
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1) ...(4)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1) ...(4)
COCATION: (1) ...(4)
LOCATION: (1) ...(4)
COTHER INFORMATION: Synthesized Peptide
US-10-619-520-4
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| NAME/KEY: PEPTIDE
| LOCATION: (1)...(4)
| OTHER INFORMATION: Synthesized Peptide
US-10-619-520-5
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Best Local Similarity
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NAME/KEY: PEPTIDE
LOCATION: (1)...(4)
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GENERAL INFORMATION:

APPLICANT: VAN HEERDE, GEORGE V.

APPLICANT: VAN HEERDE, GEORGE V.

APPLICANT: VAN HEINDE, GEORGE V.

APPLICANT: WAN BLAY.

APPLICANT: BOUWSTRA, JAN B.

APPLICANT: MOOBROEK, ANDREAS

APPLICANT: WIND RICHELE D.

APPLICANT: WIND RICHELE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: PREPARATION THEREOF

TITLE OF INVENTION: SUITABLE SOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: DIAGRAMMER: US/10/342,331

CURRENT APPLICATION NUMBER: US/10/342,331

CURRENT APPLICATION NUMBER: 2003-01-15
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TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: agents
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/10/722,075
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US/06/960,054A
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.0%; Score 18; DB 15; 1 Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 3; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US/09/219,849
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/10722075 Publication No. US20040141922A1 GENERAL INFORMATION:
                                              Sequence 14, Application US/10342331
Publication No. US20030229205A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Murine sp. US-10-342-331-14
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US-10-722-075-30
                            JS-10-342-331-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4;
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                            Indels
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                                                                                                                                                                                                                                             Sequence 151, Application US/10029206A
Publication No. US20030119720A1
GENERAL INFORMATION:
APPLICANT: Khan, Nisar A.
APPLICANT: Benner, Robert
TITLE OF INVENTION: 01igopeptide treatment of anthrax
FILE REFERENCE: 2183-5222US
CURRENT APPLICATION NUMBER: US/10/029,206A
CURRENT FILING DATE: 2001-12-21
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US-10-396-073-1

Sequence 1, Application US/10396073

Sequence 1, Deplication US/10396073

Publication No. US20030207330A1

GENERAL INFORMATION:

APPLICANT: Wescott, Charles R.

TITLE OF INVENTION: FIBRINGEN BINDING MOIETIES

FILE REFERENCE: DXX-036.1 DXX-036.1 US

CURRENT FILING DATE: 2003-03-25

PRIOR FILING DATE: 2003-03-26

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin version 3.2

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     100.0%; Pred. No. 1.2e+06;
tive 0; Mismatches 0;
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72.0%; Score 18; DB 14; L
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 175
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 151
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                          3; Conservative
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Best Local Similarity
Matches 3; Conserv
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US-10-029-206A-151
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     Sequence 57, Application US/10198677

Publication No. US20030119023A1

GENERAL INFORMATION:
APPLICANT: CHOO, Yen

APPLICANT: KLUG, Aaron

APPLICANT: MOORE, MICHAEL

ITILE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY

TITLE OF INVENTION: MOLECULES

TITLE OF INVENTION: MORECULES

TITLE OF IN
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Sequence 59, Application US/10198677

Publication No. US20030119023A1

GENERAL INFORMATION:
APPLICANT: CHOO, Yen
APPLICANT: KING, Aaron
APPLICANT: MOORE, Michael
TITLE OF INVENTION: PLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
TITLE OF INVENTION: PLEXIBLE LINKERS CONNECTED NUCLEIC ACID BINDING
TITLE OF INVENTION: MOLECULES
TITLE OF INVENTION: MOLECULES
TITLE OF INVENTION: MOLECULES
TITLE OF SEFERENCE: 8325-2011 / G11-US1
CURRENT APPLICATION NUMBER: US/10/199,677

NUMBER OF SEQ ID NOS: 144

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: canonical linker; OTHER INFORMATION: sequence variant US-10-198-677-57
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CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: canonical linker
COTHER INFORMATION: sequence variant
US-10-198-677-59
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.v.
13, Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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LENGIH: 4
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Publication No. US20040039175A1

GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Monica A
APPLICANT: Papworth, Monica A
APPLICANT: Reynoids, Lindsey
APPLICANT: Isalan, Mark
APPLICANT: SADIAN, MONICA A
APPLICANT: SADIAN, MONICA A
APPLICANT: SADIAN, MARK
APPLICANT: SADIAN, MONICA A
APPLICANT SADIAN 
                                                                                                                                                                                                                                                      APPLICANT: Choo, Yen
APPLICANT: Demaison, Christophe
APPLICANT: Demaison, Christophe
APPLICANT: Demaison, Christophe
APPLICANT: Reynolds, Lindsey
APPLICANT: Reynolds, Lindsey
APPLICANT: Isalan, Mark
APPLICANT: Isalan, Mark
TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger
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; OTHER INFORMATION: canonical linker
US-10-276-608-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: canonical linker US-10-276-608-9
                                                                                             Sequence 9, Application US/10276608 Publication No. US20040039175A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial FEATURE:
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Best Local Similarity
Matches 3; Conserv
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RESULT 23
US-10-276-608-9
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, Sequence 11, Application US/09922093 ; Patent No. US2002003783A1

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RESULT 25

GENERAL INFORMATION:

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Gaps
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OTHER INFORMATION: This sequence is made up by the first four amino OTHER INFORMATION: acids of substance P.
OTHER INFORMATION: PATENTION INFORMATION:
PATENT DOCUMENT NUMBER: 5891842
PATENT FILING DATE: 1996-04-12
PUBLICATION DATE: 1999-04-16
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism: This is a OTHER INFORMATION: naturally occuring amino termal peptide fragment OTHER INFORMATION: derived from substance P.
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Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10082691
; Publication No. US20030165541A1
; GENERAL INFORMATION:
; APPLICANT: Donovan: Stephen
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION PAIN
; FILE REFERENCE: D-3018
; CURRENT APPLICATION NUMBER: US/10/082,691
; CURRENT FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4;
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Pred. No. 1.2e+06;
1; Mismatches 0;
                                                                                                                                                              64.0%; Score 16; DB 12;
66.7%; Pred. No. 1.2e+06;
iive 1; Mismatches 0
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ORGANISM: Unknown Organism
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Best Local Similarity 66...
2, Conservative
                                                                                                                                                                                                                    Conservative
                                                           TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-154-332-2
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                                                                                                                                   Query Match
Best Local Similarity
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NAME/KEY: MOD RES
LOCATION: (1)..(4)
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PAGES: 1309-1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL: Nature
VOLUME: 262
PAGES: 784-785
                                                                                                                                                                                                                                                                    2 PRP 4
                                                                                                                                                                                                                                                                                                                  2 PKP 4
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US-10-082-691-11
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                SEQ ID NO 2
                                           LENGIH: 4
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US-10-154-332-2
US-10-154-332-2
Sequence 2, Application US/10154332
Publication No. US20030225010A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION OF PROLIFERATIC
TITLE OF INVENTION OF PROLIFERATIC
TITLE OF INVENTION OF PROLIFERATIC
CURRENT APPLICATION UMBER: US/10/154,332
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
. OTHER INFORMATION: Description of Unknown Organism: This is a naturally occuring am
; OTHER INFORMATION: ino thermal peptide fragment derived from substance P.
US-09-922-093-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Unknown Organism: This is a naturally occuring am; OTHER INFORMATION: ino thermal peptide fragment derived from substance P. US-09-938-112-11
TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain FILE REFERENCE: D-2875CIP2
CURRENT APPLICATION NUMBER: US/09/922,093
CURRENT FILING DATE: 2001-08-03
PRIOR PAPLICATION NUMBER: US 09/625,098
PRIOR APPLICATION NUMBER: US 09/489,667
PRIOR APPLICATION NUMBER: US 09/489,667
PRIOR PILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09938112
Patent No. US20020066699A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Donovan, Stephen
TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
TITLE OF INVENTION: Clostridial Toxin Derivatives and Methods for Treating Pain
CURRENT APPLICATION NUMBER: US/09/938,112
CURRENT FILING DATE: 2001-08-23
FRIOR APPLICATION NUMBER: US 09/489,667
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
LENGTH: 4
LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 9; Length 4;
Pred. No. 1.2e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 64.0%; Score 16; DB 9; Length 4; Best Local Similarity 66.7%; Pred. No. 1.2e+06; Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative 1
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APPLICANT: Hamm, Heidid
APPLICANT: Gilchrist, Annette
APPLICANT: Gilchrist, Annette
TILE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor Si
FILE REPERRNCE: 2661-101
CURRENT APPLICATION NUMBER: US/09/852,910
CURRENT APPLICATION DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US 60/275,472
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 271
SOFTWARE: Patentin version 3.0
SEQ ID NO 158
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APPLICANT: Choo, Yen
APPLICANT: Demaison, Christophe
APPLICANT: Demaison, Michael
APPLICANT: Papworth, Monika A
APPLICANT: Reynolds, Lindsey
APPLICANT: Reynolds, Lindsey
APPLICANT: Isalan, Mark
TITLE OF INVENTION: Proteins
TITLE OF INVENTION: Proteins
TITLE OF INVENTION: Proteins
GURRENT APPLICANTON WORDLAIS/00US (G13-US)
CURRENT APPLICANTON NUMBER: US/10/276,608
CURRENT FILING DATE: 2002-11-07
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn version 3.2
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// LOCATION: (1).7(4)
// OTHER INFORMATION: amino acid residues 7-10 of UGTIAl as shown in Figure 4
US-10-250-508-30
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                                                                                                                Score 16; DB 16; Length 4;
Pred. No. 1.2e+06;
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LOCATION: (1).7(4)
OTHER INFORMATION: G alpha t library linker sequence
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Pred. No. 1.2e+06;
                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: canonical linker
                                                                                                                                                                                                                                                                                                                                                                     US-09-852-910-158
i. Sequence 158, Application US/09852910
i. Publication No. US20030096297A1
j. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                      64.0%;
75.0%;
                                                                                                                Query Match
Best Local Similarity 75.0
Matches 3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 2, Conservative
NAME/KEY: MISC_FEATURE
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ORGANISM: Artificial
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| Sequence 30, Application US/10250508
| Sequence 30, Application US/10213274|
| Sequence 30, Application No US200401213274|
| SEQUENCE 30, Application No US200401213274|
| SERNEAL INFORMATION: Michael APPLICANT: Strassburg, Christian APPLICANT: Strassburg, Christian APPLICANT: Michael Gr. Predicting the Potential Risk of Carcino TITLE OF INVENTION: Inflammatory Bowel Diseases and Relevant Tests | TILE REFERENCE: 03100178aa | US/10/250,508 |
| FILE REPERENCE: 03100178aa | US/10/250,508 |
| FRIOR PELICATION NUMBER: DC 103 | PRIOR APPLICATION NUMBER: PC70 DE02/00003 |
| PRIOR FILING DATE: 2002-01-03 |
| PRIOR FILING DATE: 2001-01-05 |
| NUMBER OF SEQ ID NOS: 57 |
| SOFTWARE: PatentIn version 3.2
                     CORRESPONDENCE ADDRESS:
CORRESPONDENCE Patera L. Pabet
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlana
CITY: Atlana
CITY: Atlana
CITY: Add a
CONTRY: USA
CONTRY: USA
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 27-Max-2003
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REGISTRACTION NUMBER: 31,284
TELECOMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 15;
Pred. No. 1.2e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/867,819
FILING DATE: APRIL 13, 1992
APPLICATION NUMBER: 07/648_205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472_947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-10-376-121A-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 133
SEQUENCE CHARACTERISTICS:
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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Best Local Similarity 75.0'
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ORGANISM: Homo sapiens
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Causey, Stuart
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 50.0%;
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 Best Local Similarity 50.03
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                          1 GPRP 4
                                                                                          1 GEKP 4
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                                                                                                                                                 RESULT 37
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                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Modulation of Viral Gene Expression by Engineered Zinc Finger TITLE OF INVENTION: Proteins FILE REFERENCE: SAB1-035/00US (G13-US)
CURRENT APPLICATION NUMBER: US/10/276,608
NUMBER OF SEQ ID NOS: 163
SOFTWARE: Patentin version 3.2
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APPLICANT: Rabo, Carl O.

APPLICANT: Rabo, Carl O.

TILLE OF INVENTION: Poly Zinc Finger Proteins With Improved Linkers

FILE REPERENCE: 101496-002510US

CURRENT APPLICATION NUMBER: US/10/146,221

FRIOR APPLICATION NUMBER: US/09/260,629

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 24

SOOTWARE: Patentin Ver. 2.0

SEQ ID NO 20
                                                                           Gaps
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                                    Length 4;
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                                                                         1; Indels
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                                  Score 14; DB 12;
Pred. No. 1.2e+06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                    APPLICANT: Choo, Yen
APPLICANT: Demaison, Christophe
APPLICANT: Moore, Michael
APPLICANT: Papworth, Monika A
APPLICANT: Reynolds, Lindsey
APPLICANT: Ullman, Christopher G
APPLICANT: Isalan, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: canonical linker
                                                                                                                                                                                                                                    Sequence 12, Application US/10276608
Publication No. US20040039175A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10146221
Publication No. US20020173006A1
GENERAL INFORMATION:
APPLICANT: Kim, Jin-Soo
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                                  56.0%;
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ORGANISM: Artificial Sequence
             Query Match
Best Local Similarity 50.v.
2; Conservative
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Best Local Similarity 50.0
Matches 2, Conservative
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                                                                                                                             GEKP 4
                                                                                                          1 GPRP 4
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US-10-276-608-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4
TYPE: PRT
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TITLE OF INVENTION: No. US20030083464Alel Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr Hobbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,986
FILING DATE: 12-Mar-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/444,791

RILING DATE: 22-No. US20030083464A1-1999

APPLICATION NUMBER: US 08/482,085

FILING DATE: 07-UN-1995

APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US 08/053,049

FILING DATE: 22-APR-1993

APPLICATION NUMBER: US 08/053,049

FILING DATE: 22-APR-1993

APPLICATION NUMBER: US 07/114,618

FILING DATE: 04-NOV-1986

FILING DATE: 04-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
Pred. No. 1.2e+06;
1; Mismatches 1;
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;
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-096-986-7
                                                                                                                                                                                                                                                                   Sequence 7, Application US/10096986
Publication No. US20030083464A1
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
Richardson, Charles
Chambers, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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us-09-931-009a-2.closed.rapb

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Sequence 158, Application US/10411336A

Sequence 158, Application US/10411336A

Sequence 158, Application US. US2004001858A1

GENERAL INPORMATION:

APPLICANT: GLICKRIST, ANNETTE

APPLICANT: HAWM, HELDI

TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR

TITLE OF INVENTION: METHOD FOR 108111,336A

CURRENT APPLICATION NUMBER: US/10/411,336A

CURRENT FILING DATE: 2003-04-11

PRIOR APPLICATION NUMBER: US 60/275472

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

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GENERAL INFORMATION:

APPLICANT: Britles, David E

APPLICANT: McDaniel, Larry S

APPLICANT: Watarlo, Edwin

APPLICANT: Crain, Marilyn J

APPLICANT: Crain, Marilyn J

APPLICANT: Tart, Rebeca, Susan

APPLICANT: Tart, Rebeca, Susan

APPLICANT: Tart, Nebeca, Susan

APPLICANT: Brocks-Walter, Alexis

TITLE OF INVENITON: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF

TITLE OF INVENITON: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF

FILE REPERBUES: 57903361

CURRENT FILING DATE: 2002-11-19

PRIOR APPLICATION NUMBER: 08/529,055

PRIOR FILING DATE: 1996-09-15

NUMBER OF SEQ ID NOS: 111

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: G alpha t library linker sequence US-10-411-336A-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Streptococcus pneumoniae US-10-299-636-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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US-10-198-677-58
US-10-198-677-58
Sequence 58, Application US/10198677
Publication No. US20030119023A1
GENERAL INFORMATION:
APPLICANT: GTOO, Yen
APPLICANT: KIUG, Aaron
TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY
TITLE OF INVENTION: MOLECULES
GURRENT APLICATION NUMBER: US/10/198,677
CURRENT FILING DATE: 2002-07-17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 58
LENGTH: 4
                                                                                                                                                                          Sequence 56, Application US/10198677

Sequence 56, Application US/10198677

Publication No. US20030119023A1

GENERAL INFORMATION:

APPLICANT: GHOO, Yen

APPLICANT: MOORE, Michael

APPLICANT: MOORE, Michael

TITLE OF INVENTION: NUCLEIC ACID BINDING POLYPEPTIDES CHARACTERIZED BY

TITLE OF INVENTION: NUCLEIC ACID BINDING

TITLE OF INVENTION: MOLECULES

FILE REFERENCE: 8325-2011 / G11-US1

CURRENT APPLICATION NUMBER: US/10/198,677

CURRENT FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 144

SOFTWARE: PATCHIN VEr. 2.0

SEQ ID NO 56
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// OTHER INFORMATION: Description of Artificial Sequence: canonical linker
// OTHER INFORMATION: sequence variant
US-10-198-6777-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGNILSM: Artificial Sequence
FEATURE:
CHER INFORMATION: Description of Artificial Sequence: canonical linker
US-10-198-677-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.0%; Score 14; DB 14; Length 4; 50.0%; Pred. No. 1.2e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0%;
Matches 2; Conservative 1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.0
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GPRP 4
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2 PRP 4
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TYPE: PRT (CRGANISM: synthetic construct US-09-836-433-15)
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ORGANISM: unknown organism
                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 2; Conserv
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            1 GP 2
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US-09-836-433-16
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                                                                                                                                                                                 SEQ ID NO 15
LENGTH: 2
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; Publication No. US20040162232A1
; Publication No. US20040162232A1
; Publication No. US2004016223A1
; APPLICANT: Halth, Matrix Sciences
; APPLICANT: Mitts, Thomas
; APPLICANT: Jimenez, Felipe
; TITLE REFERENCE: LEASTIN DIGEST COMPOSITIONS AND METHODS UTILIZING SAME
; FILE REFERENCE: 126595.101
; CURRENT APPLICATION NUMBER: US/10/778,253
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447461
; PRIOR RILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.2
; LENGTH: 4
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                                                                                                             APPLICANT: McDaniel, Larry S
APPLICANT: Swiatlo, Edwin
APPLICANT: Swiatlo, Edwin
APPLICANT: Swiatlo, Edwin
APPLICANT: Crain, Marilyn J
APPLICANT: Crain, Marilyn J
APPLICANT: Tart, Rebecca
APPLICANT: Hollingshead, Susan
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: PNEUMOCOCCAL SURFACE PROTEINS AND USES THEREOF
FILE REFERRORS: 5790/361
CURRENT APPLICATION NUMBER: US/10/299,636
CURRENT FILING DATE: 1996-09-16
PRIOR PFLING DATE: 1996-09-16
PRIOR FILING DATE: 1996-09-15
PRIOR FILING DATE: 1996-09-15
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 111
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Pred. No. 1.2e+06;
0; Mismatches 1;
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                                   Sequence 111, Application US/10299636
Publication No. US20040077847A1
APPLICANT: Briles, David E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 15, Application US/09836433 ; Publication No. US20030049797A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pneumoniae US-10-299-636-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative.
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US-10-778-253-36
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                 JS-10-299-636-111
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US-10-778-253-36
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US-09-836-433-15
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APPLICATI' YOLI, YORINALAL
APPLICATI' YOLI, YORINALAL
APPLICATI' YOLI, YORINALAL
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RESULT 50

US-10-232-838-3

Sequence 3. Septication US/10232838

Publication No. US2003064053A1

GENERAL INFORMATION:
APPLICANT: Liu, Shengjiang

APPLICANT: Liu, Dayou

TILLE OF INVENTION: MULTIVALENT PROTEIN CONJUGATE WITH MULTIPLE LIGAND-BINDING DOMAINE;
TILLE OF INVENTION: RECEPTORS

FILE REFERENCE: 26050-707

CURRENT APPLICATION NUMBER: US/1/0/232,838

CURRENT APPLICATION NUMBER: US 6/316,718

PRIOR APPLICATION NUMBER: US 6/316,718

PRIOR PRING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.1

FINDER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 192, Application US/10363208
Publication No. US20040048243A1
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
FILE REFERENCE: 065774.P005PCT
CURRENT APPLICATION NUMBER: US/10/363,208
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 273
SSOTEMARE: PatentIn version 3.1
LENGTH: 3
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                                                                                                                Length 3;
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                                                                                                          Query Match 52.0%; Score 13; DB 12; Length 3; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/TET: Peptide
; LOCATION: (1)..(3)
; OTHER INFORMATION: synthetic construct
US-10-363-208-192
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial sequence
FEATURE:
          ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-346-198-64
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US-09-755-630A-277
i Sequence 277, Application US/09755630A
i Sequence 277, Application US/09755630A
i Publication No. US20030194399A1
i GENERAL INFORMATION:
APPLICANT: ALBHAI, MURTAZE F.
APPLICANT: ARTWOOD, JAMES D.
APPLICANT: SAMPSON, HUGH A.
APPLICANT: MARMERTERS, CHARLES A.
ITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
FILE REFERENCE: 11899.0217.NPUSON (MOBIZI7)
CURRENT APPLICATION NUMBER: US/09/755,630A
CURRENT FILING DATE: 2000-01-05
PRIOR PELICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 293
SOFTWARE: Patentin Version 3.0
SEQ ID NO 277
TENDAMEN: PARMER PATENTING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 293
SEQ ID NO 277
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VS-10-346-198-64

Sequence 64, Application US/10346198

Publication No. US20040043485A1

GENERAL INFORMATION:
APPLICANT: WISSLER, SUSAN R.
APPLICANT: JANG, NING
APPLICANT: JANG, ZHRONG
APPLICANT: ZHANG, XIAROYU
APPLICANT: ZHANG, XIAROYU
APPLICANT: JEDY, SEAN R.
ITITLE OF INVENTION: TANNSPOSABLE ELEMENTS IN RICE AND METHODS OF USE
ILLE REFERENCE: 18465-1018
CURRENT APPLICATION NUMBER: US/10/346,198
CURRENT APPLICATION NUMBER: 60/337,409
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 64
LENGTH: 3
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                                                                                                                                                                                                                                                             Length 3;
                                                                                                                                                                                                                                                        Query Match 52.0%; Score 13; DB 10; I
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/836,433;
CURRENT FILING DATE: 2001-04-16;
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0;
SEQ ID NO 16
LENGTH: 3
TYPE: PT
TYPE: PT
ORGANISM: synthetic construct
US-09-836-433-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Synthetic polypeptide US-09-755-630A-277
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ORGANISM: Artificial Sequence
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1 GP 2

Search completed: September 7, 2004, 19:36:05 Job time: 123 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	using sw model	<pre>September 7, 2004, 18:56:12 ; Search time 39 Seconds (without alignments) 9.866 Million cell updates/sec</pre>
Copyright	OM protein - protein search, using sw model	Run on: September 7

US-09-931-009A-2 25 1 GPRP 4	BLOSUM62 Gapop 10.0 , Gapext 0.5
Title: Perfect score: Sequence:	Scoring table:

283366

283366 segs, 96191526 residues

Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65 summaries Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	proline-rich antib	4,	ı ED		0	rRNA N-glycosidase	7	venom basic protei	- 53	hypothetical prote	4	ď	in		-	_	hypothetical prote	꿏	sarcosine oxidase	hypothetical prote		· O	, "	NADH2 dehydrogenas	nicotinic acetylch	nicotinic acetylch	hypothetical prote	glucose transporte	synaptobrevin SNB-
SUMMARIES	CI	874112	A34259	NAXAB	149627	153690	S16486	A36589	S19327	S02055	PN0644	A96650	T22081	801718	JQ1356	F87163	T36074	AC3515	AC3075	F98211	E72581	H96003	-	w	S37068	A41384	138	E72707	A44887	(7)
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	Length	30	42	49	57	58	28	59	62	64	99	70	72	79	84	87	90	90	91	91	92	93	95	σı	0	О	0	105	0	0
dŧ	Query Match		100.0	100.0		100.0	00	100.0	100.0	100.0	100.0	100.0	100.0	8	100.0	100.0	100.0	8	8	100.0	8	100.0	8	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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09 2 F7266	11 2 8727	11 2 D7264	15 2 T3462	17 2 T2198	19 2 86985	19 2 G7272	24 2 T0324	25 2 D7224	25 2 T0352	27 2 A4926	27 2 D7559	27 2 E8725	29 2 T3629	31 2 T0797	32 2 A8329	33 2 T0408	34 2 A4095	34	34 2 B9820	34 2 T5060	35 2 81254	37 2 T1560	40 2 G9660	43 2 AI083	44 1 JN0	44 2 87142	44 2 T0356	44 2 D8315	45 1 TNLJB	45 2 H7526	49 2 F726	50 2 F706	50 2 T4685	51 2 A691	53 2 AB271
5 100.0	25 100.0 1	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.	5 100.0	5 100.0	5 100.0	5 100.0	5. 100.0	5 100.0	5 100.0	5 100.0	100.0	5 100.0	5 100.0	5 100.0	5 100.0	5 100.0	100.0	5 100.0	5 100.0
30	31	32	33	34	35	36	37	38	. 39	40	41	42	43	44	45	46	47	48	49	20	51	52	23	54	22	26	57	28	6	09	61	62	63	64	65

ALIGNMENTS

RESULT 1 974112 proline-rich antibacterial protein - green crab (fragment) C;Species: Carcinus maenas (green crab, common shore crab) C;bate: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998 C;Accession: S74112
R;Schnapp, D.; Kemp, G.D.; Smith, V.J. Eur. J. Biochem. 240, 532-539, 1996 A;Title: Purification and characterization of a proline-rich antibacterial peptide, A;Title: Purification and characterization of A;Title: S74112; MUD:97008941; PMID:8856051 A;Reference number: S74112 A;Rocession: S74112 A;Rocious: 1-30 cSCH> A;Residues: 1-30 cSCH> A;Residues: antibacterial C;Keywords: antibacterial
Query Match Best Local Similarity. 100.0%; Pred. No. 85; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GPRP 4
RESULT 2 A34259

with

cytochrome P450mt4, phenobarbital-inducible, mitochondrial, hepatic - rat (fragment) N;Contains: oxidoreductase (EC 1.....)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Mar-1999
C;Accession: A34259

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Dactenedin 7 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius
C;Accession: A36589
B;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
B;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
A;Title: Aino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of A;Reference number: A36589; MUID:91035404; PMID:2229048
A;Accession: A36589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S16486
R;Montecucchi, P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, F.; Soria, M.; Lappi, D. Int. J. Pept. Protein Res. 33, 263-267, 1989
A;Title: N-terminal sequence of some ribosome-inactivating proteins.
A;Reference number: S16331; MUID:89326691; PMID:2753596
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                                                                                                                                                                                                                                                                                                        cytochrome P450 2B15 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug.1996 #sequence_revision 02-Aug-1996 #text_change 11-Jun-1999
C;Accession: 153690
R;Nakayama, K.; Suwa, Y.; Mizukami, Y.; Sogawa, K.; Pujii-Kuriyama, Y.
Gene 136, 333-336, 1993
A;Title: Cloning and sequencing of a novel rat cytochrome P450 2B-encoding g
A;Reference number: 153690; MUID:94124025; PMID:8294026
A;Accession: 153690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rRNA N-glycosidase (EC 3.2.2.22) 5b - common soapwort (fragment)
N.Alternate names: ribosome-inactivating protein SO-5b; saporin 5b
C.Species: Saponaria officinalis (common soapwort)
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 10-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                               Gaps
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A,Molecule type: DNA
A,Residues: 1-58 <RES-
A,Cross-references: GB:D17343; NID:g468474; PIDN:BAA04162.1; PID:g468475
C,Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C,Keywords: heme; transmembrane protein
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A,Residues: 1-58 <MON>
C,Superfamily: rRNA N-91ycosidase; rRNA N-glycosidase homology
C,Exporfamily: rRNA N-91ycosidase
F,6-58/Domain: rRNA N-glycosidase homology (fragment) <RNG>
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100.0%; Score 25; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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                      Pred. No. 1.6e+02;
Mismatches 0;
100.08; Fig.
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Best Local Similarity 100.0%;
Matches 4; Conservative 0.
                      Best Local Similarity 100. Matches 4; Conservative
                                                                                                                                                                        33 GPRP 36
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C;Species: Anthopleura xanthogrammica (giant green sea anemone)
C;Species: Anthopleura xanthogrammica (giant green sea anemone)
C;Date: 31: Nav-1981 #sequence revision 30-Jun-1987 #text_change 04-Oct-1996
C;Date: 31: A92547; A94482; A01795
R;Reimer, N.S.; Yssunobu, C.L.; Yssunobu, K.T.; Norton, T.R.
A;Title: Amino acid sequence of the Anthopleura xanthogrammica heart stimulant, anthoole A;Reference number: A92547
A;Anthopleule type: protein
A;Accession: A92547
A;Molecule type: protein
A;Residues: 1-49 cRE1>
R;Bennett, C.D.
R;Bennett, C.D.
A;Reference number: A94482
A;Accession: A94482
A;Accession: A94482
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Aaces (2.7ul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jun-1999
C;Aaces sion: 149627
R;Lakso, M.; Masaki, R.; Noshiro, M.; Negishi, M.
R;Lakso, M.; Masaki, R.; Noshiro, M.; Negishi, M.
A;Title: Structures and characterization of sex-specific mouse cytochrome P-450 genes as A;Reference number: 149625; MUID:91146586; PMID:1997326
                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-42 <SHA>
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; mitochondrion; monooxygenase; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 1-11,'PN',14-24,'A',26-28 <BEN>
C;Comment: Anthopleurin B is the most potent peptide heart stimulator isolated from the
C;Superfamily: sea anemone toxin
C;Keywords: cardiotoxin
F;4-46,6-36,29-47/Disulfide bonds: #status predicted
                                                            Biochémistry 29, 866-873, 1990
A;Title: A phenobarbital-inducible hepatic mitochondrial cytochrome P-450 immunochemical
A;Reference number: A34259; MUID:90254127; PMID:2340279
A;Accession: A34259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: 16aoh-c
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: heme; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                     Length 42;
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                                                                                                                                                                                                                                                                                                                           ; Score 25; DB 2; Length 42; Pred. No. 1.2e+02; 0; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-57 <RES>
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Best Local Similarity 100.0%;
Matches 4; Conservative 0.
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Best Local Similarity 100.
Matches 4; Conservative
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A;Accession: I49627

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Query Match

us-09-931-009a-2.open.rpr

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Apported. Fimported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cjactes Arabidopsis thaliana (mouse-ear cress)
Cjactes Ozymar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
Cjaccession: A6650
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ajuubors: Hunter, J.L.; Junkor, L.; Alaubors: Hunter, J.L.; Junkor, M.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Enwis, J.; Julu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Affile: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Recossion: A66500
A;Status: preliminary
A;Accession: A6650
A;Cross-references: GB:AE005173; NID:97940276; PIDN:AAF70835.1; GSPDB:GN00141
C;Accession: PN0644

#wray Ur., L.V.; Flaher, S.H.

Gene 130, 145-150, 1993

A;Title: The Streptomyces coelicolor glnR gene encodes a protein similar to other bacteri
A;Refearence number: UN0831; MUID:93345814; PMID:7688332

A;Accession: PN0644

A;Molecule type: DNA
A;Residues: 1-66 < WRA>
A;Residues: 1-66 < WRA>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F41E7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T22081
R;Lennard, N.
R;Lennard, N.
R;Lennard, N.
R;Accession: T22081
A;Reference number: Z19509
A;Residues: 1-72 < WIL>
A;Residues: 1-72 < WIL>
A;Residues: 1-72 < WIL>
A;Residues: Company (CAA92131.1; GSPDB:GN00028; CESP:F41E7.8)
A;Comerimental source: Clone F41E7
C;Genetics:
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100.0%; Score 25; DB 2; Length 70
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 25; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 4; Conservative 0; Mismatches 0;
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A,Map position: 1
C,Superfamily: hydroxyproline-rich glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               venome basic proteinase inhibitor - leaf-nosed viper
N.Alternate names: trypsin inhibitor (Kunitz-type)
C;Species: Eristocophis macmahoni (leaf-nosed viper)
C;Abccies: Eristocophis macmahoni (leaf-nosed viper)
C;Abcciesion: S19327
R;Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A;Rieferonce number: S19327; MuID:92077130; PMID:1743283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-62 <SID>
C/Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C/Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
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C;Species: Streptomyces coelicolor
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Score 25; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                             Query Match 100.0%; Score 25; DB 2; Length 59; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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A,Status: preliminary
A,Molecule type: protein
A,Resdiucs: 1-59 < FRA
C,Superfamily: cathelin; cystatin homology
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Query Match Best Local Similarity Matches 4; Conserv

A; Gene: CESP: F41E7.8 A; Map position: X A; Introns: 18/2

41 GPRP 44

1 GPRP 4

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eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A.Title: Massive gene decay in the leprosy bacillus.
A.Accession: F87163
A.Accession: F87163
A.Accession: Proliminary
A.Molecule type: DNA
A.Residues: 1-87 <STO>
A.Gonesios: 1-87 <STO>
A.Gonesios: A.Gonesios:
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AC3515
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C'Species: Streptomyces coelicolor
C'Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C'Accession: T36074
C'Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21573
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A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE126.04
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A;Molecule type: DNA
A;Residues: 1-90 «KUR»
A;Cross-references: GB:AE008918; PIDN:AAL53286.1; PID:g17984169; GSPDB:GN00191
A;Experimental source: strain 16M
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100.0%; Pred. No. 2.4e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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%;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-90 < OLI>
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Matches 4; Conservative 0;
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C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: F87163
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Balbiani ring protein 1-gamma (clone pCp28) - midge (Chironomus pallidivittatus) (fragme C;Species: Chironomus pallidivittatus
C;Species: Chironomus pallidivittatus
C;Species: Os-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 17-Mar-2000
C;Accession: S01718
R;Lendahl, U.; Saiga, H.; Hoeoeg, C.; Edstroem, J.E.; Wieslander, L.
Genetics 117, 43-49, 1987
A;Titles: Rapid and concerted evolution of repeat units in a Balbiani ring gene.
A;Reference number: S01717
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Cypatesion: J01356; J00919
Rychacesion: J01356; J00919
J. Gen. Virol. 72, 2325-2331, 1991
J. Gen. Virol. 72, 2325-2331, 1991
A;Fitle: The nucleotide sequence and genome structure of the geminivirus miscanthus stre
A;Reference number: J01355; MUID:92013947; PMID:1919519
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;Comment: Miscanthus streak virus causes leaf streak.
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A;Note: the authors translated the codon AGA for residue 30 as Lys
C;Superfamily: unassigned Balbiani ring proteins
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100.0%; Pred. No. 2.2e+02;
.ive 0; Mismatches 0; Indels
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Query Match Best Local Similarity Matches 4; Conserv

7 GPRP 10

RESULT 14

JQ1356

1 GPRP 4

A; Molecule type: mRNA A; Residues: 1-79 < LEN>

Query Match Best Local Similarity

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GPRP 62

RESULT 15

1 GPRP 4

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A, Molecule type: DNA A, Residues: 1-84 <CHA> A, Cross-references: DDE C, Comment: Miscanthus &

GPRP 87

RESULT

1 GPRP 4

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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Nolecule type: DNA
A;Residuae: 1-93 xCNB-
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, N.A.; Jones, T. A; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, R.W.; Jones, T.
Bcience 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. DNA Res. 6, 83-1101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr. A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: E72581
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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand R;Finan, T.M.; Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing endos A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: H96003
                                                                                                                                                                                                                                                                                               A;Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80938.1; PID:d1044724; PID:g5108 A;Experimental source: strain K1 C;Genetics: A;Gene: APES065
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C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-92 <KAW>
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C;Accession: E72581
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                                                                                                                                                                                                                                                                                                                                             C,Accession: AC3075
R,Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell & Xerp, P.; Romero, P.; Zhang, S.
Science 294, 2.317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                      - Agrobacterium tumefaciens (strain C58, Dupo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE008689; PIDN:AAL45017.1; PID:g17742678; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                sarcosine oxidase delta subunit [imported] - Agrobacterium tumefaciens (stri
C,Species: Agrobacterium tumefaciens
C,Date: il-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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100.0%; Pred. No. 2.4e+02;
viematches 0; Indels
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E72581
hypothetical protein APES065 - Aeropyrum pernix (strain X1)
C;Species: Aeropyrum pernix
C;Date: 20-Ang-1ee ages 20-Ang-1ee
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100.0%; Score 25; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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A,Map position: linear chromosome
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11 GPRP 14

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1 GPRP 4

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-91 <KUR>

C, Genetics: A, Gene: soxD

A; Accession: AC3075

Conservative

GPRP 14

11

a

8

1 GPRP 4

Query Match Best Local Similarity

C; Genetics:

h 100.0%; Score 25; DB 2; I Similarity 100.0%; Pred. No. 2.5e+02; 4; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 4; Conserv

1 GPRP 4

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GPRP 8

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dicotinic acetylcholine receptor alpha chain - Chinese cobra (fragment)

(Species: Naja naja atra (Chinese cobra)

(Joate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

(Joacession: A41384

R;Neumann, D.; Barchan, D.; Horowitz, M.; Kochva, E.; Fuchs, S.

Proc. Natl. Acad. Sci. US.A. 86, 7255-7259, 1989

A;Title: Snake acetylcholine receptor: cloning of the domain containing the four extracel A;Reference number: A41384; MUID:89386720; PMID:2780569
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrt A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nicotinic acetylcholine receptor alpha chain - checkered water snake (fragment)
C;Species: Narrix tessellata (checkered water snake)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C;Accession: B41384
R;Neumann, D.; Barchan, D.; Horowitz, M.; Kochva, E.; Fuchs, S.
R;Neumann, D.; Barchan, D.; Horowitz, M.; Kochva, E.; Fuchs, S.
A;Title: Snake acetylcholine receptor: cloning of the domain containing the four extracel A;Reference number: A41384; MUID:89386720; PMID:2780569
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A;Residues: DBJ:AP000060; NID:g5104188; PIDN:BAA80061.1; PID:d1043847; PID:g5104
A;Experimental source: strain K1
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C,Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor
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A;Residues: 1-104 <NEU>
A;Cross-references: GB-MX6389; NID:g213378; PIDN:AAA49387.1; PID:g213379
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor
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100.0%; Score 25; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 25; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0;
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A,Molecule type: mRNA
A,Residues: 1-104 <NEU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Thiosphaera pantotropha
C;Date: 27-Oct-1995 #sequence_revision 26-Jul-1996 #text_change 08-Oct-1999
C;Accession: S56134; S50166
R;Berxks, B.C.; Archardson, D.J.; Reilly, A.; Willis, A.C.; Ferguson, S.J.
Biochem. J. 309, 983-992, 1995
A;Title: The napEDABC gene cluster encoding the periplasmic nitrate reductase system of A;Reference number: S56128; MUID:95365980; PMID:7639719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:236773; NID:9600089; PIDN:CAA85349.1; PID:9600096
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; NAD; oxidoreductase; transmembrane protein
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*Residues: 1-101 < WEI>-
A,Cross-references: EMBL:X68301; NID:g444012; PIDN:CAA48370.1; PID:g397908
A,Experimental source: strain AN387
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A;Molecule type: mRNA
*Residues: 1-95 <LEN>
A;Cross-reference: EMBL:X06431; NID:g7016; PID:g683545
A;Note: the authors translated the codon AGA for residue 42 as Lys
C;Superfamily: unassigned Balbiani ring proteins
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        Length 95;
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A;Accession: $38320
A;Status: preliminary
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A;Residues: 1-97 <BER>

A, Molecule type: DNA

48 GPRP 51

1 GPRP 4

8

Query Match Best Local Similarity Matches 4; Conserv

54 GPRP 57

qq

1 GPRP 4

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hypothetical protein APE0602 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72646
C;Bararabayasi, V; Huno, V; Horikawa, H; Yamazaki, S; Haikawa, V; Jin-no, K; Takahawa, H; Takamiya, M; Masuda, S; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; K, DNA, Res. 6, 83-101, 1999
A;Tile: Complete gnome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrian A;Reference number: A72450; MuID:99310339; PMID:10382966
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: F7266
R;Rawarabayaei, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawarabayaei, Y.; Hino, Y.; Horikawa, H.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa, H.; Takamiya; M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa, Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr. A;Mitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr. A;Molecule number: A7266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 < KAM>A;Cross_references: DDBJ;Ap000060; NID:g5104188; PIDN:BAA79734.1; PID:d1043520; PID:g5104A;Cross_references: Strain KI
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A;Residues: 1-111 «KAM»
A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79572.1; PID:d1043358; PID:g5104
A;Experimental source: strain K1
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A,Start codon: GTG
C,Superfamily: Mycobacterium leprae adenine phosphoriboxyltransferase homolog apt2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S72737
A; Status: preliminary
A; Modecule type: DNA
A; Residues: 1-111 < SMI>A; Residues: 1-110 < SMI>Cross-references: EMBL: U00011; NID: 9466807; PIDN: AAA17101.1; PID: 9466826
C; Genetics:
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100.0%; Score 25; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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C,Superfamily: Aeropyrum pernix hypothetical protein APE0757
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R;Smith, D.R.; Robison, K.
submitted to the BMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1177.
A;Reference number: $72694
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                      Glucose transporter isoform 1, GLUT 1 - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Species: Jr Feb-1994 #sequence_revision 17-Feb-1994 #text_change 24-Sep-1999
C,Accession: A44887
R,Hogan, A.; Heyner, S.; Charron, M.J.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Th
Pevelopment 113, 363-372, 1991
A,Fitle: Glucose transporter gene expression in early mouse embryos.
A,Reference number: A44887; MUD:92111400; PMID:1765007
A,Accession: A44887
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-107 < HQG>
A,Accession: A4887
A,Experimental source: embryo
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R; Greco, T.; Bradshaw, H.; O'Brien, D.
submitted to the EMBL Data Library, May 1998
A; Description: The Sequence of C. elegans cosmid T10H9.
A; Reference number: Z21306
A; Accession: T33239
A; Status: pre-liminary; translated from GB/EMBL/DDBJ
A; Status: pre-liminary; translated from GB/EMBL/DDBJ
A; Residues: 1-109 -GRE>
A; Residues: 1-109 -GRE>
A; Experimental source: SmBL; AF067949; PIDN: AAC19234.1; GSPDB: GN00023; CESP: T10H9.4
A; Experimental source: strain Bristol N2; clone T10H9
A; Genetics:
A; Genetics:
A; Map position: 5
A; Introns: 39/3
C; Superfamily: synaptobrevin
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
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                                                                                          Gaps
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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                          Length 105;
                                                                                   Indels
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                       Query Match 100.0%; Score 25; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
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C;Species: Ae
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Matches
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A; Status: preliminary
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R,Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, June 1999
A;Reference number: 221549
A;Reference number: T34629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-115 <SAU-
A;Residues: 1-115 <SAU-
A;Residues: BMBL:AL078618; FIDN:CAB44536.1; GSPDB:GN00070; SCOEDB:SC10A7.26
A;Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                  hypothetical protein SC10A7.26 - Streptomyces coelicolor
C,Species: Streptomyces coelicolor
C,Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F39B2.6 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C.Accession: T21988
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hypothetical protein YMR294w-a - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
                                                                        Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 25; DB 2; Length 115; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                Query Match
100.0%; Score 25; DB 2; L.
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dobson, R. ubmitted to the EMBL Data Library, March 1997; Reference number: Z19498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :Introns: 61/1
:Superfamily: rat ribosomal protein S26
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A;Map position: 1
A;Introns: 61/1
C,Genetics:
A,Gene: APE0602
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C;Species: Acropyrum permix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: G72725
R;Kawarassion: G72725
R;Kawarassion: Y; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K; Takaha awa, H; Takamaya, M; Masuda, S; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Ki DiNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn A;Reference number: A72450; MUID:99310339; PMID:10382966
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R;Nantel, A.; Quatzano, R.S.
B;Nantel, A.; Quatzano, R.S.
A;Title: Charcterization of three rice basic/leucine zipper factors, including two inhit A;Reference number: Z14856; MUID:97094901; PMID:8940135
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A;Residues: 1.119 «KAM»
A;Cross-references: DDBS:AP000059; NID:g5103911; PIDN:BAA79299.1; PID:d1043085; PID:g510:
A;Experimental source: strain K1
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C;Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 24-Nov-1999
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C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                  A;Gene: MIPS:YMR294w-a
A;Map position: 13R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YMR294w-a
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A,Note: osZIP-2a
C;Keywords: DNA binding; leucine zipper; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 119;
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                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X80836; GSPDB:GN00013; MIPS:YMR294w-a
C;Genetics:
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Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0;
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A;Molecule type: mRNA
A;Residues: 1-124 <NAN>
                  Cyaccession: S6980
R/Badcock, K.; Churcher, C.
Submitted to the EMBL Data Library, August 1994
A/Accession: S6980
A/Accession: S6980
A/Accession: S6980
A/Rocale type: DNA
A/Residues: 1-119 < BAD>
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100.0%; Score 25; DB 2; Length 124;

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R; Pote, K.G.; Hauer III, C.R.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Kretsinger, R.H. Biochemistry 32, 5017-5024, 1993
A;Title: Otcocin.22, the major protein of aragonitic frog otcocnia, is a homolog of phos A;Reference number: A49269; MUID:99264410; PMID:8494877
A;Rodession: A49269
A;Status: preliminary
A;Rodecule type: protein
A;Residues: 1-127 <POT>
A;Rodecule type: protein
A;Rote; K.G.
in NASA Space Biology, Halstead, T.W., ed., pp.205-209, NASA Office of Space Science and A;Reference number: A23737
A;Status: preliminary
A;Accession: A23737
A;Status: protein
A;Residues: 1-19, X., 21-45, X., 47-50, XNDQX', 51-74, 'Q', 76-80, 88-112, 'X', 114-115, 'Y', 117-1 C;Superfamily: phospholipase A2
F;26-120, 28-44, 43-99, 49-127, 50-92, 59-85, 78-90/Disulfide bonds: #status predicted
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Cibace: 03-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
Cibace: 03-Jec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
Cibacession: D75595
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F.White, O.; Eisen, J.A.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mals.; Shath, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUD:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87258
R;Accession: E87258
R;Aiderman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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X.Residues 1.127 «WH.)
A;Cross-references: GB.AE001862; GB.AE001825; NID:g6460468; PIDN:AAF12374.1; PID:g6460666
A;Experimental source: strain Rl
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A;Map position: 2
C;Superfamily: Deinococcus radiodurans hypothetical protein DRA0026
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Best Local Similarity 100...
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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-125 cARN>
A;Residues: 1-125 cARN>
A;Cross-references: GB:AE001798; GB:AE000512; NID:g4982033; PIDN:AAD36543.1; PID:g498204
A;Experimental source: strain MSB8
C;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Genetics:
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571
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Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16182.1; PID:g3128330
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C;Species: Rhodobacter capsulatus
C;Accession: T03229
R;Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M. Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulation to the chromosome of Rhodobacter capsulation T03529
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 12-Jun-2003
C;Accession: D72247
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                                                                Indels
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                         Pred. No. 3.2e+02;
Mismatches 0;
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100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0;
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                     Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
4; Conserv?
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Residues: 1-125 <VLC>
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A,Status: preliminary
A,Molecule type: DNA
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A; Accession: E87258

0; Mismatches

100.0%; 100.0%;

Query Match
Best Local Similarity 100.
Matches 4; Conservative

35 GPRP 38

1 GPRP 4

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Conserved hypothetical protein PA2827 [imported] - Pseudomonas aeruginosa (strain PAO1) (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Psep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 (Speciesion: A83293 Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.W.
Nature 406, 959-964, 2000 Aprille: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog A; Reference number: A82950; MUID:20437337; PMID:10984043
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C;Species: Rattus norregicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C;Accession: A40886; A40959; A32694; A32544
S;Itch, N.; Furnya, T.; Ozaki, K.; Ohta, M.; Kawasaki, T.
J. Biol. Chem. 266, 12595-12598, 1991
A;Title: The secretin precursor gene. Structure of the coding region and expression in the A;Reference number: A40886; MUID:91286291; PMID:2061329
A;Reference number: A40886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-132 <STO>
A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06215.1; GSPDB:GN001:
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R;Nakamura, I.; Kameya, N.; Aoki, T.; Tada, T.; Norita, E.; Kanzaki, H.; Uchimiya, H.
R;Nakamura, I.; Kameya, N.; Aoki, T.; Tada, T.; Norita, E.; Kanzaki, H.; Uchimiya, H.
A;Description: cBMB bata Library, August 1994
A;Description: cDNA sequence of ribosomal protein S31 homolog from rice calli exposed to A;Reference number: 215193
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C.Species: Oryza sativa (rice)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
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100.0%; Score 25; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 3.4e+02;
Conservative 0; Mismatches 0:
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A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Rebiudes: 1-133 < ANAK
A,Rebiudes: 1-133 < ANAK
A,Experimental: 1-133 < ANAK
A,Experimental: source: SMBL:D38011; PIDN:BAA07208.1
C,Experimental: source: subsp. Japonica, callus
C,Superfamily: rat ribosomal protein S26
C,Keywords: ribosome
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C,Superfamily: hypothetical protein YCL033c
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A;Molecule type: DNA
A;Residues: 1-134 <ITO>
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(Species: Streptomyces coelicolor
(Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Nov-2000
(SAccession: T36299
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A)Cross-references: EMBL:AL049819, PIDN:CAB42676.1; GSPDB:GN00070; SCOEDB:SCE7.17c
A)Experimental source: strain A3(2)
C)Genetics:
A,Gene: SCOEDB:SCE7.17c
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
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                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-127 <STO>
A;Cross-references: GB:AE005673; NID:g13421177; PIDN:AAK22065.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0078
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-131 < BME.
A;Cross-references: BURD:
A;Cross-references: BURD:
A;Experimental source: strain WT 137
C;Superfamily: Chlamydomonas reinhardtii low CO2-inducible 14.2K protein
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100.0%; Score 25; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

A; Accession: T36299

48 GPRP 51

RESULT 44

1 GPRP 4

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73 GPRP 76
1 GPRP 4
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RESULT 45

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hypothetical protein AGR L 1189 [imported] - Agrobacterium tumefaciens (strain C58, Cerec; Species: Agrobacterium tumefaciens
C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: B98206
A; Liu, F; Wollam, C; Allinger, M; Doughty, D; Scott, C; Lappas, C; Markelz, B; Science 294, 2332-2328, 2001
A; Liu, F; Wollam, C; Allinger, M; Doughty, D; Scott, C; Lappas, C; Markelz, B; A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUD:21608551; PMID:11743194
A;Accession: B98206
A;Status: preliminary
A;Mesidues: 1-134 <KUR>
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C,Species: Homo sapiens (man)
C,Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
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R;Kochrer, K.; Beyer, A.; Mewes, H.W.; Weil, B.; Wiemann, S. submitted to the Protein Sequence Database, June 2000
A;Reference number: Z25141
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C,Genetics:
A,Note: DKFZp434I1016.1
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Similarity 100.0%; Pred. No. 3.5e+02;
4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.5e+02;
ative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 4, Conservative
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Job time : 42 secs
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: mRNA
A;Residues: 1-134 <AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 GPRP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 ĠPŔP 122
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       R;Kopin, A.S.; Wheeler, M.B.; Nishitani, J.; McBride, E.W.; Chang, T.; Chey, W.Y.; Leite Proc. Natl. Acad. Sci. U.S.A. 88, 5335-5339, 1991
A;Title: The secretin gene: evolutionary history, alternative splicing, and developmenta A;Reference number: A40959; MUID:91271384; PMID:1711228
A;Accession: A40959
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Agrobacterium tumefaciens
C;Date: 11.-Jan-2002 #sequence_revision 11.-Jan-2002 #text_change 18-Nov-2002
C;Date: 11.-Jan-2002 #sequence_revision 11.-Jan-2002 #text_change 18-Nov-2002
C;Accession AG3080
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
R;Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Mosidues: 1-134 <XOD2>
A;Mosidues: 1-134 <XOD2>
A;Cross-references: GB:M31495; NID:g206887; PIDN:AAA42126.1; PID:g206888
B;Goss-references: GB:M31495; NID:g206887; PIDN:AAA42126.1; PID:g206888
B;Goss-references: GB:M31495; NID:g206887; PMC:; Rathe, J.; Cauvin, A.; Robberech
A;Title: Isolation and primary structure of rat secretin.
A;Reference number: A32544; MUID:89246545; PMID:2719704
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                                                                                                                                                                                                                   A;Molecule type: DNA,
Msesidues: 1.13 4KOP-
A;Kesidues: 1.13 4KOP-
A;Cross-references: 1.13 4KOP-
A;Cross-references: GB:M64033; NID:g206891; PIDN:AAA42128.1; PID:g206892
R;Kopin, A.S.; Wheeler, M.B.; Leiter, A.B.
R;Kopin, A.S.; Wheeler, M.S.; A. 2799-2331, 1990
A;Title: Secretin: structure of the precursor and tissue distribution of the mRNA.
A;Reference number: A35094; MUID:90192795; PMID:2315322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Cross-references: GB:AE008689; PIDN:AAL45061.1; PID:g17742726; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
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; Score 25; DB 2; I; Pred. No. 3.5e+02; 0; Mismatches

100.0%;

Conservative

116 GPRP 119

1 GPRP 4

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Query Match
Best Local Similarity

A, Molecule type: protein A, Residues: 33-59 <GOS> C, Superfamily: glucagon C, Keywords: duplication

Status: preliminary

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Gaps

. 0

100.0%; Score 25; DB 2; Length 134; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels

A; Map position: linear chromosome

A;Status: preliminary A;Molecule type: DNA

Query Match Best Local Similarity 100...

102 GPRP 105

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4

RESULT . B98206

1 GPRP 4

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xylella fas
ictalurid h
canis famil
coryza sativ
homo sapien
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 33, Last annotation update)
FMRFamide-like neuropeptide AF9.
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Bukaryota, Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
NCBI_TaxID=6253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cowden C., Stretton A.O.W.;
"Eight novel FWRFamide-like neuropeptides isolated from the nematode Ascaris suum.";
Peptides 16:491-500(1995).
-i- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
Query Match
100.0%; Score 25; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
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MOD_RES 9 9 AMIDATION.

SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;
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NUSB XYLPA
VG09 HSV11
VG09 HSV11
VGC7 HUWAN
PGC7 HUWAN
PGC7 HUWAN
PACA CHICK
APIT BOVIN
APIT BOVIN
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SEQUENCE.
MEDLINE=95380362; PubMed=7651904;
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 GPRP 4
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FAR9_ASCSU
ID FAR9_ASCSU
AC P43172;
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                                                                                                           September 7, 2004, 18:45:46; Search time 23 Seconds (without alignments) 9.056 Million cell updates/sec
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P01231
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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APAS ANTXA
TYAB ANTXA
IVBT_ERIMA
VG18 BPWU
VIA1 MYCTU
YNAC_PARPN
PRRP_BOVIN
PRRP_BOVIN
RNL2 BIV06
ACHĀ NAJNA
VET7 BIV06
ACHĀ NAJNA
NSL2 PIG
GGCC HUMAN
RS13 THEWA
ACHA NATTE
PA2H XENLA
MSRB LEPIN
MSRB METTH
KNLI HUMLT
RS6 AGRT5
SODC HUMLT
RS6 AGRT5
SODC HUMLT
RS6 AGRT5
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Maximum Match 100%
Listing first 65 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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rhizobium m rhizobium s rhodobacter homo sapien pseudomonas

deinococcus mus musculu mycobacteri

gallus gall homo sapien m heart- an

mus musculu

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Gaps

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5274 MW;
                                                                                                  Cnidocyst; 3D-structure.
DISULRID 4 46
DISULRID 6 36
                                                                                                                                                                                                                                                  4; Conservative
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4 7
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                                                                                                            STRUCTURE BY NMR.
MEDIATE=56027101; PubMed=7582896;
MEDIATE=56027101; PubMed=7582896;
Monks S.A., Pallaghy P.K., Scanlon M.J., Norton R.S.;
"Solution structure of the cardiostimulant polypeptide anthopleurin-B and comparison with anthopleurin-A.";
Structure 3:791-803(1995).
-!- FUNCTION: Binds specifically to the sodium channel, thereby
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
01-JAV-1988 (Rel. 06, Last sequence update)
10-OCT-2003 (Rel. 06, Last sequence update)
Anthopleurin B (Toxin AP-B).
Anthopleura xanthogrammica (Giant green sea anemone).
Bukaryota; Metazoa; Gnidaria; Anthozoa; Zoantharia; Actiniaria;
Nymantheae; Actiniidae; Anthopleura.
                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=85261226; PubMed=4019448; Reimer N.S., Yasunobu K.T., Norton T.R.; Reimer N.S., Yasunobu C.L., Yasunobu K.T., Norton T.R.; Amino acid sequence of the Anthopleura xanthogrammica heart
             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 43, Last aequence update)
Antibacterial 6:5 Kba protein (Fragment).
Carcinus maenas (Common shore crab) (Green crab).
Edwaryota, Metazoa, Arthropoda, Crustacea, Malacostraca, Bucarida, Decapoda, Placospenata, Brachyura, Portunoidea; Portunidae, Carcinus.
                                                                                                                                                                                                                                                   Score 25; DB 1; Length 30;
Pred. No. 34;
0; Mismatches 0; Indels
                                                                                                                                                                                                                          30 30 30 30 30 AA; 3305 MW; 6E2C2205934896C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                  49 AA.
30 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stimulant, anthopleurin-B.";
J. Biol. Chem. 260:8690-8693(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=81090973; PubMed=6108877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bennett C.D.;
Unpublished results, cited by:
                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                    4; Conservative
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STANDARD;
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Best Local Similarity
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                                                                                    NCBI TaxID=6759;
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Siddigi A.R., Zaidi Z.H., Joernvall H., "Purification and characterization of a Kunitz-type trypsin inhibitor
                                                                                                                                                                                                         PIR; A92547; NAXAB.
PDB; 1APF; 11-JUL-96.
INTERPO; IPR000693; Anenome_toxin.
PFam; PF00706; toxin 4; 1.
Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
delaying its inactivation during signal transduction. Thus it strongly stimulates mammalian cardiac muscle contraction.
--- SUBCELLULAR LOCATION: Secreted; cnidocyst.
--- MISCELLANEOUS: Anthopleurin B is the most potent peptide heart stimulator isolated from the sea anemone.
---- SIMILARITY: Belongs to the sea anemone sodium channel inhibitory toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last sequence update)
02-FEB-2003 (Rel. 41, Last annotation update)
Venom trypsin inhibitor.
Eristocophis macmahoni (Leaf-nosed viper)
Eristocophis Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Eristocophis.
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PRINTS; PR00759; BASICPTASE.
ProDoom; PD000222; Kunitz BPT1; 1.
SWART; SM00131; KU; 1.
PROSITE; PS00280; BPT1 KUNITZ 1; 1.
PROSITE; PS0279; BPT1 KUNITZ 2; 1.
Serine protease inhibitor.
DISULFID 2 52
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interPro; IPR002223; Kunitz_BPTI.
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                                                                                                                                                              MEDINE=91141314; PubMed=1981088; MEDINE=91141314; PubMed=1981088; MCADINE=91141314; PubMed=1981088; MCADINE=91141314; PubMed=19810., van Scolingen D., Zainuddin Z.F., Catty D., van Emben J.D.A., Dale J.W.; "Characterization of a Mycobacterium tuberculosis insertion sequence belonging to the IS3 family."; Mol. Microbiol. 4:1607-1613 (1990).
-!- SIMILARITY: STRONG, TO M.TUBERCULOSIS INSERTION ELEMENT IS6110 HYPOTHETICAL 12.0 kDa PROTEIN.
     30-MAY-2000 (Rel. 39, Last annotation update)
Insertion element IS986 hypothetical 8.2 kDa protein (ORFA1)
                                                                      Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 74; 100.0%; Pred. No. 83; 1. Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Transposable element.
SEQUENCE 74 AA; 8232 MW; 2700FA99DD4C9745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X52471; CAA36708.1; -.
                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                        NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 GPRP 69
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Q56353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@igb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Priess H., Brauer B., Schmidt C., Kamp D.; "Sequence of the left end of Mu."; In Symonds N., Toussaint A., van de Putte P., Howe M.M. (eds.); Phage Mu. pp.277-296, Cold Spring Harbor Laboratory Press, New York (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21920971; PubMed=11922669;
Morgan G.J., Hatfull G.F., Casjens S., Hendrix R.W.;
"Bacteriophage Mu genome sequence: analysis and comparison with
Mu.like prophages in Haemophilus, Neisseria and Deinococcus.";
J. Mol. Biol. 317;337-359(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
Mu-like viruses.
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REACTIVE BOND (BY SIMILARITY)
0A2ED0ADB20DF938 CRC64;
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                                                                        1; Length 62;
                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stoddard S.F., Howe M.M.;
Submitted (SEP-1987) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8444 MW; B29272F519B8E068 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical protein gpl8 (B18 protein).
                                                                   100.0%; Score 25; DB 100.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                   72 AA
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(Rel. 17, Last sequence update)
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12 13
62 AA; 6772 MW;
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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Best Local Similarity
                                                                                            Local Similarity
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Stoddard S.F., How
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 AA;
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SEQUENCE 72
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YIA1 MYCTU
ID YIA1 MYCTU
AC P19771;
DT 01-FEB-1991
DT 01-FEB-1991
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01-FEB-1991
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Q38625;
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ACT SITE
SEQUENCE
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Matches
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VG18 BRND
ID T 16-0C
DT 16-0C

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINSAUCS 35512 / LMD 82.5;
MEDLINE-95366880; PubMed=7639719;
Berks B.C., Richardson D.J., Reilly A., Willis A.C., Ferguson S.J.;
"The napBDABC gene cluster encoding the periplasmic nitrate reductase system of Thiosphaera pantotropha.";
Biochem. J. 309:983-992(1995).
                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Hypothetical protein in napC 3'region (Fragment).
Paracoccus pantotrophus (Thiosphaera pantotropha).
Bacteria, Proteobacteria, Alphaproteobacteria; Rhodobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 AA; 10325 MW; B50B4E2C6BD38127 CRC64;
97 AA
PRT;
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LT 8 BOVIN

Matches

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                                                                                                                                                                                                                                                                                                                                                                  peptide-RNA complex.";
Science 270:1200-1203(1995).
-!- FUNCTION: Transcriptional regulator that acts by binding to the
-trans-activating responsive sequence (TAR) RNA element and
activates transcription initiation and/or elongation from the LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-89386720; PubMed=2780569;
Neumann D., Barchan D., Horowitz M., Kochva E., Fuchs S.;
Neumann D., Barchan D., Horowitz M., Kochva E., Fuchs S.;
Snake acetylcholine receptor: cloning of the domain containing the four extracellular cysteines 86;
Proc. Natl. Acad. Sci. U.S.A. 86;7255-7259(1989).
-i- FUNCTION: After binding acetylcholine, the AChR responds by an
                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-90221985; PubMed=2183467;
MEDLINE-90221985, DubMed=2183467;
Survey K.J., Oberste M.S., Blser J.E., Braun M.J., Gonda M.A.;
"Nucleotide sequence and genome organization of biologically active proviruses of the bovine immunodeficiency-like virus.";
Virology 175:391-409(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Elapidae, Elapinae, Naja.
                                                                                                                                                                                                                                                                                                    MEDLINE=96072972; PubMed=7502045;
Puglisi J.D., Chen L., Blanchard S., Frankel A.D.;
"Solution structure of a bovine immunodeficiency virus Tat-TAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h
Similarity 100.0%; Pred. No. 1.2e+02;
4; Conservative 0; Mismatches 0; Indels
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01-07N-1990 (Rel. 13, Last sequence update)
01-07N-1990 (Rel. 14, Last sequence update)
Acceylcholine receptor protein, alpha chain (Fragment)
Naja naja (Indian cobra)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 AA; 11739 MW; 28479ED907F06A55 CRC64;
                         Bovine immunodeficiency virus (isolate 106) (BIV).
Viruses, Retroid viruses; Retroviridae, Lentivirus.
NCBI_TaxID=11658;
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PDB; 1BIV; 23-DEC-96.
PDB; 1MNB; 27-JAN-97.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV; M3Z691; SORF$BIV106.
InterPro; IPR001831; IV_Tat.
Pfam; PF00539; Tat; 1.
                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 68-81.
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Best Local Similarity
Matches 4; Conserv
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

-!- TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION (G-54 PROVIDE AMIDE GROUP). 08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
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Hormone; Amidation; Signal; Cleavage on pair of basic residues.
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                    Length 97;
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01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
TAT protein (Transactivating regulatory protein) (S ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                              0; Indels
                  Score 25; DB 1; L
Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
100.0%; Scc. No. 4...
100.0%; Pred. No. 4...
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                                                                                                                                                                                                                                                                 PRT;
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10544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 releasing peptide PrRP20].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
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33
58
53
98 AA;
                       Query Match
Best Local Similarity
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                                                                                                                                                    48 GPRP 51
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P19564;
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SEQUENCE
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RESULT 9
TAT_BIV06

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Gaps

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SEQUENCE
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MOD_RES
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                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENE outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                           SUBUNIT: Pentamer of two alpha chains, and one each of the beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96249586; PubMed=8815087;
Forslund O., Hansson B.G.;
"Human papillomavirus type 70 genome cloned from overlapping PCR
products: complete nucleotide sequence and genomic organization.";
J. Clin. Microbiol. 34:802-809(1996).
                                                                                                 delta, and gamma chains.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION.
N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M26388; AA449384.1; -.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006202; Neur chan LBD.
Pfam; PF002931; Neur chan LBD; 1.
PRINTS; PR00252; NRIONCHÂNNEL.
PROSTITE; P800236; NEUROTR ION CHANNEL; 1.

Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 1; Length 104; 100.0%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 70.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VGBI_TaxID=39457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12194 MW; 47A39E2C9BFBA7A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Best Local Similarity luv.
4; Conservative
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24
75
104
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VET HPV70
AC PS0785;
DT 01-0CT-1996
DT 28-FEB-2003
DE E7.
CS Human papil
CC Papillomavi
CX NCBL TAXID=
RN KI SEQUENCE FR
RX MEDLINE-962
RA FOFELUMD 0.
RT TOTALINE 962
RT FORDINE-97
RT PLOMUCE:
RT PLOMUCE:
RT PLOMUCE:
RT PLOMUCE:
RT PLOMUCE FR
RY SEQUENCE FR
RY MEDLINE-962
RA FORDINE-962
RA FORDINE-962
RA FORDINE-962
RA FORDINE-962
RT TAYONOVEL
RY TAYONOVEL

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DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kininogen-2 precursor (BMK-2) [Contains: Maximakinin; Bradykinin; Maximakinin associated peptide].

Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).

Bukaryota; Metazoa; Chondata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Archeobatrachia; Bombina.

NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ440236; CAD29346.1; -.
Amphibian defense peptide; Vasodilator; Bradykinin; Repeat; Signal;
Amidation; Pyrrolidone carboxylic acid; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRADYKININ.
MAXIMAKININ POTENTIATING PEPTIDE.
MAXIMAKININ EARBOXYLIC ACID.
AMIDATION (G-114 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Skin secretion, and Venom gland;
MEDLINE=22830826; PubMed=12948837;
Chen T., Bjourson A.J., McClean S., Orr D.F., O'Kane E.J., Rao P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning of maximakinin precursor cDNAs from Chinese toad, Bombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 77-95 AND 105-114, AMIDATION, AND VARIANT LEU-74.
                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      maxima, venom.";
Peptides 24:853-861(2003).
-!- FUNCTION: Potent vasodilator. Binds B1 and B2 bradykinin
                                                                                                                                                                                                                                                                                                 Length 109;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51D4525AB970C853 CRC64;
                                                                                                                                                                                                                                                             2FD3C643DFAFF891 CRC64;
                                                                                               EMBL; U21941; AAC54851.1; -.
EMBL; U22461; AAC54881.1; -.
InterPro; IPR00048; Papvi_B7.
Emry Protect; Ex; I.
Early protect; Transcription regulation; Oncogene; DNA-binding; Trans-acting factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- TISSUE SPECIFICITY: Skin.
-i- SIMILARITY: Belongs to the bradykinin family.
                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 1; I
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 41, Last sequence update) (Rel. 43, Last annotation update)
                                                                                                                                                                                                                     C-XX-C MOTIF-1.
C-XX-C MOTIF-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAXIMAKININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KININOGEN-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 F
13361 MW;
                                                                                                                                                                                                                                                             109 AA; 12657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
Les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptors.
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15-MAR-2004
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P83055;
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O62786;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the S26E family of ribosomal proteins.
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                 Length 114;
                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dobson R.; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA; 13249 MW; OFB79092B80B605D CRC64;
               100.0%; Score 25; DB 1; I 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 1; I
100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                               10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
80S ribosomal protein $26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF01283; Ribosomal S26e, 1.
PROSITE, PS00733; RIBOSOWAL S26E; FALSE_NEG.
                                                                                                                                                                                                                                            117 AA.
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                                                        0; Mismatches
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SEQUENCE FROM N.A.
Canty J.M., Young R.F., Fallavollita J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WormPep; F39B2.6; CE16012.
InterPro; IPR000892; Ribosomal_S26E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Glucose transporter type 2, liver)
SLC2A2 OR GLUT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z92834; CAB07387.1; -. PIR; T21988; T21988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                        4; Conservative
                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribosomal protein.
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                                                                                                                                      85 GPRP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9823;
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                                                                                                                                                                                                                                            CAEEL
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062786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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045499;
                                                                                                                                                                                               RESULT 13
RS26_CABEL
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GTR2 PIG
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Mallya M., Campbell R.D., Aguado B.;
"Transcriptional analysis of a novel cluster of LY-6 family members in the buman and mouse major histocompatibility complex: five genes with many splice forms.";
                     FUNCTION: Facilitative glucose transporter. This isoform likely mediates the bidirectional transfer of glucose across the plasma membrane of hepatocytes and is responsible for uptake of glucose by the beta cells; may comprise part of the glucose-sensing mechanism of the beta cell; may also participate with the Na(+)/Glucose cotransporter in the transcellular transport of glucose in the small intestine and kidney (By similarity). SIMELLARIAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to the sugar transporter family. Glucose transporter subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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16-OCT-2001.(Rel. 40, Last sequence update)
18-PEB-2003 (Rel. 41, Last annotation update)
Lymphocyte antigen 6 complex locus G6C protein precursor (Protein
NG24).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO05829; Sug_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003682; Sugat_transpt.
Pfam; PF00083; Sugat_tr; 1.
PRINTS; PR00171; SUGRIRNSPORT.
PROSITE; PS50850; MFS; 1.
PROSITE; PS50821; SUGAR_TRANSPORT_1; PARTIAL.
PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
TRANSMEMDTANE; Sugar_transport; Transport; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; Length 12
100.0%; Pred. No. 1.3e+02;
rive 0: Mismatches 0; Indels
(MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
10 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13503 MW; DSF73168DBF03203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
11 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF054835; AAC12737.1; -. InterPro; IPR007114; MFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LY6G6C OR NG24 OR C6ORF24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
4; Conserv?
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120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LG6C HUMAN
095867;
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DOMAIN
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TRANSMEM
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SEQUENCE
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LG6C HUMAN
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                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                      sites (By similarity).
-!- SUBUNIT: Part of the 30S ribosomal subunit. Forms a loose heteroidiner with protein S19. Forms two bridges to the 50S subunit in the 70S ribosome (By similarity).
-!- SIMILARITY: Belongs to the S13P family of ribosomal proteins.
implicated in subunit movement. Contacts the tRNAs in the A and P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-074/1990 (Rel. 13, Created)
01-077-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain (Fragment).
Natrix tessellata (Dice snake) (Checkered water snake).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes; Colubroidea, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00416; Ribosomal_S13; T.
PRODOM; PD001363; Ribosomal_S13; 1.
PROSITE; PS004646; RIBOSOMAL_S13_1; 1.
PROSITE; PS004046; RIBOSOMAL_S13_2; 1.
Ribosomal protein; RNA-binding; rRNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 AA; 14432 MW; 55E66FDF6FA16097 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 1; I
100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               475; -.
01315; -; 1.
_IPR001892; Ribosomal_S13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89386720; PubMed=2780569;
                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001798; AAD36543.1; -. PIR; D72247; D72247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                            FIGR; TM1475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACHA NATTE
                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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MEDLINE=99287316; PubMed=1036071;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Mett D.H., Hickey E.K., Preterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Octron M.D., Pratt M.S., Phillips C.A., Richardson D.,

A Heidelberg J., Sutton G.G., Flaischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,

Theidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.";

Thymorrows sequence of Thermotoga maritima.";

Nature 399:323-229(1999)

C. - FUNCTION: Located at the top of the head of the 30S subunit, it contacts several helices of the 16S rRNA. In the 70S ribosome it contacts the 23S rRNA (bridge Bla) and protein L5 of the 50S subunit (bridge Blb), connecting the 2 subunits; these bridges are
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                           Shina S., Tamiya G., Oka A., Inoko H., Shina S., Tamiya G., Oka A., Inoko H., Shina S., Tamiya G., Oka A., Inoko H., Subron sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."; Submitted (SpE-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: SOME, TO LY-6/UPAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYMPHOCYTE ANTIGEN 6 COMPLEX LOCUS G6C
                                                                                            Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J., Lasky S., Hood L., "Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                           Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A., Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; Length 125, 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                        region.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9ED7549894C71311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF129756; AAD18076.1; -...
EMBL; AP000504; BAB63379.1; -..
Genew; HGNC:13936; LY6G6C.
Signal.
1 18 PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ315533; CAC85539.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30S ribosomal protein S13.
     Genomics 80:113-123 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
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Q9X1I5;
30-MAY-2000 (Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2000 (Rel. 39, 5-MAR-2004 (Rel. 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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NCBI_TaxID=2336;
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                                                    SEQUENCE
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Matches

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RESULT 16
RES13 THEMA
RS13 THEMA
RS13 THEMA
AC 09X1I5
DD 30-MAX
DT 15-MAX
DD 30-MAX
DD 30-MAX
DD 30-MAX
RS13 THEMA
RS 115-MAX
RS THEMA
RS THEMA
RS NEIGHT
RA HAEL
RA RAEL
RA R

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us-09-931-009a-2.open.rsp

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InterPro; IPR001211; PhospholipaseA2.
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TIGRFAMs; TIGR00357; 1.
Oxidoreductase; Complete proteome.
                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   122 GPRP 125
                                                                                                                                                                                                                                1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=173;
                                                                    Glycoprotein.
DISULFID
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DISULFID
DISULFID
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MSRB LEPIN
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                                                                                                                   EXTRACELLULAR.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION.
CONFERS TOXIN RESISTANCE (POTENTIAL).
CONFERS TOXIN RESISTANCE (POTENTIAL).
CONFERS TOXIN RESISTANCE (POTENTIAL).
N.LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOR-2004 (Rel. 43, Last annotation update)
Phospholipase A2 homolog otoconin-22 (Oc22).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93264410, PubMed=8494877;
Pote K.G., Hauer C.R. III, Michel H., Shabanowitz J., Hunt D.F., Kretsinger R.H.;
                                                                                                                                                                                                                                                                                                     ;
0
                                     PIR; B41384; B41384.
InterPro; IPR006202; Neur chan LBD.
InterPro; IPR006201; Neur chan LBD.
PFam; PF02331; Neur chan LBD; 1.
PRINTS; PR00252; NRIONCHÂNNEL.
PROSTIE; PS00236; NEUROTR ION CHANNEL; 1.

NON_TER 1
                                                                                                                                                                                                                                                                                 Length 127;
                                                                                                                                                                                                -> H (IN REF. 1; AAA60451).
-> W (IN REF. 1; AAA60451).
-> N (IN REF. 1; AAA60451).
-> D (IN REF. 1; AAA60451).
                                                                                                                 >127

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BY -> H (IN REF. 1; AAA60451)

Y -> H (IN REF. 1; AAA60451)

Y -> N (IN REF. 1; AAA60451)

CONFERS TOXIN REF. 1; AAA60451)
                                                                                                                                                                                                                                                                                                   0; Indels
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                           PRT; 127 AA.
                                                                                                                                                                                                                                                                                                   0; Mismatches
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                100.0%;
100.0%;
                   EMBL; M26389; AAA49387.1; -. EMBL; M30045; AAA60451.1; -.
                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A49269; A49269.
HSSP; P00593; 4BP2.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                         67 GPRP 70
                                                                                                                                                                                                                                                                                                                       1 GPRP 4
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                                                                                                                             DISULFID
                                                                                                                                                                                                                                        CONFLICT
NON TER
SEQUENCE
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CARBOHYD
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PA2H_XENLA
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SEQUENCE FROM N.A.

STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;

MEDLINE=22598143; PubMed=12712204;

Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-G., Jia J., Tu Y.-F.,

Jiang J.-X., Qu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qlan Z., Wang S.-Y., Ma W.,

Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.;

"Unique physiological and pathogenic features of Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interrogan revealed by whole-genome sequencing.";
Nature 422:888-893(2003).
-!- CAPALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin protein L-methionine S-oxide + reduced thioredoxin.
-!- SIMILARITY: Belongs to the msrB Met sulfoxide reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 1; Length 12
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                 BY SIMILARITY.
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
W, 996A448766859BCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6)
MSRB OR LA0824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
Pfam; PF00068; phoslip; 1.
PRINTS; PR00389; PHPHILPASEA2.
Probom; PD000303; PhospholipaseA2; 1.
SMART; SM00085; PA2C; 1.
PROSITE; PS00118; PA2 HIS; FALSE_NEG.
PROSITE; PS00119; PA2_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE011268; AAN48023.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
ilarity 100.0%;
Conservative 0
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InterPro; IPR002579; DUF25.
Pfam; PF01641; SelR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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SECR_RAT
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SECR RAT
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-TROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 5592 / PAOL;

MEDLINE=20431337; PubMed=10984043;

MEDLINE=20431337; PubMed=10984043;

A stover C.K., Phem X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., A Garber R.L., Gollery L., Tolentino E., Weetbrook-Wadman S., Yuan Y., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Nopportunistic pathogen.

I copportunistic pathogen.

I nature 406:959-964 (2000).

I CATALITIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.

Protein L-methionine S-oxide + reduced thioredoxin.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                         Query Match 100.0%; Score 25; DB 1; Length 132; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 25; DB 1; Length 132; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                            Q91016;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pepcide methionine sulfoxide reductase msrB (EC 1.8.4.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AE004709; AAG06215.1; -.
PIR; A83293; A83293.
HAMAP; MF 01400; -; 1.
HAMAP; MF 01400; -; 1.
Figh: PF016A1; SelR; 1.
ProDom; PD044057; DUF25; 1.
ProDom; PD044057; DUF25; 1.
Prodom; PD04057; DUF25; 1.
Cxidoreductas; Complete proteome.
ACT SITE 119 119 BY SIMILARITY.
SEQÜENCE 132 AA; 14824 MW; 640E0ABEBEFC055A CRC64;
BY SIMILARITY.
3B9DA6715CDF55E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA.
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121 121 B
132 AA; 14848 MW;
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                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
                                                                                                                                     112 GPRP 115
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                                                                                                         1 GPRP 4
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RS26 ORYSA
ID RS26 ORYSA
                                                                                                                                                                                                                 PSEAE
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MSRB_PSEAE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=90192755; PubMed=2315322;
Kopin A.S., Wheeler M.B., Leiter A.B.;
"Secretin: structure of the precursor and tissue distribution of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDILINE=91271384; PubMed=1711228;
KOPIL M.S., Wheeler M.B., Nishitani J., McBride E.W., Chang T.M.,
Chey W.Y., Leiter A.B.;
"The secretin gene: evolutionary history, alternative splicing, and
developmental regulation.";
Proc. Natl. Acad. Sci. U.S.A. 88:5335-5339(1991).
                                                                                                                                     Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRANTECV. Japonica; TISSUE-Callus;
Nakamura I., Kameya N., Aoki T., Tada T., Norita E., Kanzaki H.,
Uchimiya H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Score 25; DB 1; Length 133; Similarity 100.0%; Pred. No. 1.5e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AA; 15016 MW; 8455305124690178 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 87:2299-2303(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELAL...
01-JUL-1989 (Rel. 11, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Secretin precursor.
P49216;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
RPS26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Program Pro1283; Ribosomal S26E.
Pfam; PF01283; Ribosomal S26e; 1.
PROSITE; PS00733; RIBOSOMAL S26E; 1.
Ribosomal Protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D38011; BAA07208.1; -. PIR; T04081; T04081. Gramene; P49216; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 GPRP 113
                                                                                                                                                                                                                                  NCBI_TaxID=4530;
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STANDARD;
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2
25
142 AA;
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Best Local Similarity
Matches 4; Conserv
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TRANSMEM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIP_MOUSE
P48756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
GIP_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                      Gossen D., Vandermeers A., Vandermeers-Piret M.-C., Rathe J.,
Cauvin A., Robberecht P., Christophe J.;
"Isolation and primary structure of rat secretin.";
Biochhem. Biophys. Res. Commun. 160.862-867(1989)
-:- FUNCTION: Stimulates formation of NaHCO(3)-rich pancreatic juice
and secretion of NaHCO(3)-rich bile and inhibits HCl production by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECRETIN.
AMIDATION (G-60 PROVIDE AMIDE GROUP).
, D9FA1A4C1F7C86E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Potassium voltage-gated channel subfamily E member 1-like protein
(AMME syndrome candidate gene 2 protein) (AMMECR2 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                      MEDLINE-91286291; PubMed-2061329;
Itoh N., Furuya T., Ozaki K., Kawasaki T.;
"The secretin precursor gene. Structure of the coding region and
expression in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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TISSUB-Neuron, and Placenta;
MEDLINE=99425266; PubMed=10493825;
Piccini M., Vitelli F., Seri M., Galietta L.J.V., Moran O.,
Bulfone A., Banfi S., Pober B., Renieri A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 1; I
100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                the stomach.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucagon family; Hormone, Amidation;
Cleavage on pair of basic residues; Signal.
SIGNAL 1 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                     J. Biol. Chem. 266:12595-12598 (1991)
                                                                                                                                                                              SEQUENCE OF 33-59.
MEDLINE=89246545; PubMed=2719704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 AM
15072 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A40886; A40859.
InterPro; IRR000532; Glucagon.
Pfam; PF00123; hormone2; 1.
SMART; SM00070; GLUCA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00260; GLUCAGON; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M31495; AAA42126.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 AA;
               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 GPRP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KC1L HUMAN
Q9UJ90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD RES
SEQUENCE
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KC1L_HUMAN
SOUTH THE SECOND DESCRIPTION OF THE SECOND D
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                                                                                                                                                                                                    MEDINE-22388257; PubMed=12477932;

MEDINE-22388257; PubMed=12477932;

MEDINE-22388257; PubMed=12477932;

MEDINE-22388257; PubMed=12477932;

MEDINE-22388257; PubMed=12477932;

MISCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MEDINE-22388257; PubMed=12477932;

MISCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MEDINE-22388257; PubMed=12477932;

MISCHUL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MEDICHORNO L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MEDICHORNO L., Modin T.B., Toshlywiki S., Carninci P., Prange C.,

MARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MARA S.S., Worley Y.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

MARING M., Sodergren B.J., Lu X., Gibbs R.A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Milting M., Madan A., Young A.C., Schwultz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schwultz J., Myers R.M.,

Menterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Menterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

Menterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

Menterfield Y.S.N., Storetten E.,

Menterfield M.S.J., John W.S.J., Whyther 
"XCNEI-like gene is deleted in AMME contiguous gene syndrome: Identification and characterization of the human and mouse homologs."; Genomics 60:251-257(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MIM; 300194; -.
GO: GO:001847; C:voltage-gated potassium channel complex; TAS.
GO; GO:0008016; P:regulation of heart rate; TAS.
Transmembrane; Glycoprotein; Alport syndrome; Deafness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 CYTOPLASMIC (POTENTIAL).
2 N-LINKED (GLCNAC. .) (POTENTIAL)
25 N-LINKED (GLCNAC. ..) (POTENTIAL)
14993 MW, EDBECG11CDEGGBFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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EMBL; BC035330; AAH35330.1; -.
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EMBL; Z19564; CAA79621.1; --
EMBL; D08831; AAA41225.1; --
EMBL; M92916; AAA41237.1; --
PIR; JN0589; JN0589.
PIR; JN0589; JN0589.
Interpro; IPR000323; Glucagon.
Pfam; PP00123; bormone2; 1.
SMART; SM00070; GLUCA, 1.
PROSITE; PS00260; GLUCAGON; 1.
Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.
SIGNAL
                                                                                                                                                                                                          SEQUENCE FROM N.A. STRSUE=Jejunum; STRAN-Sprague-Dawley; TISSUE=Jejunum; STRAN-Sprague-Dawley; TISSUE=Jejunum; MEDLINE=93189623; PubMed=8446620; Tseng C.C., Jarboe L.A., Landau S.B., Williams E.K., Wolfe M.; Tseng C.C., Jarboe L.A., Landau S.B., Williams E.K., Wolfe M.; "Insulinotropic peptide: structure of the precursor and tissue-specific expression in rat."; Proc. Natl. Acad. Sci. U.S.A. 90:1992-1996(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1132:72-74(1992).
-!- FUNCTION: Potent stimulator of insulin secretion and relatively por inhibitor of gastric acid secretion.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highly expressed in the duodenum and jejunum.
-!- SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley, TISSUE=Intestine;
MEDIINE=52379094; PubMed=1380834;
MEDIINE=52379094; PubMed=1380834;
MIGASHIMOTO Y., Liddle R.A., Simchock J.;
"Molecular cloning of rat glucose-dependent insulinotropic peptide (GIP).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
NCBI_TaxID=1061;
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nEDLINE=93119451; PubMed=1476614; Sharma S.K., Austin C., Howard A., Lo G., Nicholl C.G., Le "Characterization of rat gastric inhibitory peptide cDNA." U. Mol. Endocrinol. 9:265-272(1992).
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144 AA; 16401 MW; 091D7617459C6032 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-FBB-2003 (Rel. 41, Last annotation update)
30S_ribosomal protein S6
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36 GPRP 39
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O68126;
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RS6_RHCA
LD RS6 RS AC
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                                                                                                                                                                                                                                                                                                                                                                      P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

MEDLINE-96350462; PubMed=8764827;

NA MEDLINE-96350462; PubMed=8764827;

NA Schieldrop P.J., Galling R.W., Elliot R., Hewitt J., Kieffer T.J.,

NA Montrosh C.H.S., Pederson R.A.;

T "Isolation of a wurine glucose-dependent insulinotropic polypeptide

T "Isolation of a wurine glucose-dependent insulinotropic polypeptide

T (GIP) cDNA from a tumor cell line (STG6-14) and quantification of

T (GIP) cDNA from a tumor cell line (STG6-14) and quantification of

T Glucose-induced increases in GIP mRNA.";

T Blochim. Blophys. Act at 1308:111-113 (1996).

C -: FUNCTION: Potent simulator of insulin secretion and relatively

CC -: SUBCELULAR LOCATION: Secreted.

CC -: SUBCELULAR LOCATION: Secreted.

CC -: SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S71426; S71426.
HSSP; P01274; 1GCN.
MGD; MGI:107604; GIC.
MGD; MGI:107604; GIC.
Pfam; PF00123; hormone2; 1.
SWART; SW00070; GLUCAGON; 1.
GLUCAGON family; Hormone; Cleavage on pair of basic residues; Signal.
SIGNAL
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Gastric inhibitory polypeptide precursor (GIP) (Glucose-dependent insulinotropic polypeptide).
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144 AA; 16359 MW; 26E718665D4DA8C3 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-WAX-2004 (Rel. 43, Last annotation update)
asservic inhibitory polypeptide precursor (GIP)
insulinotropic polypeptide).
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STRAIN-Wistar; TISSUE=Duodenum;
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                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                          Fonstein M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Backer A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeeu A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Sinorhizobium meliloti strain 1021."; Sinorhizobium meliloti strain 1021."; Proc. Natl. Acad. Sci. U.S.A. 98:9977-9882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the S6P family of ribosomal proteins.
                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the S6P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                  SEQUENCE FROM N.A.
STRAIN=SB1003 / St Louis;
MEDILNE=97404404; PubMed=9256491;
Vlock C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstei "Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003.";
                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 1; Length 14; Pred. No. 1.6e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39A45DF2617143AD CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPSF OR R011138 OR SMC00568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF 00366; -; 1.
InterPro; IPR000529; Ribosomal_S6.
Pfam, PF01250; Ribosomal_S6; 1.
ProDom; PD03809; Ribosomal_S6; 1.
TIGREAMS; TIGR0166; S6; 1.
PROSITE; PS01048; RIBOSOMAL_S6; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribosomal protein; rRNA-binding.
SEQUENCE 144 AA; 16363 MW; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF010496; AAC16216.1; -. PIR; T03563; T03563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 GPRP 141
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RS6_RHIME
ID RS6_RHIME
AC Q92QZ7;
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removed. Usage by and for commercial ont (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith D.R., Doucette-Stammin.A., DeLoughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Porthier B., Olu D., Spadafora R., Vicare R., Wang W., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniells C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155 (1997).

-! CATALYIC ACTIVITY: Protein L-methionine + oxidized thioredoxin = protein L-methionine S-oxide + reduced thioredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 149;
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28-FEB-2003 (Rel. 41, Last annotation update)
Peptide methionine sulfoxide reductase msrB (EC 1.8.4.6)
                                                                                                                                                                                                                                                          Pfam; PF01250; Ribosomal_S6; 1.
ProDom; PD003809; Ribosomal_S6; 1.
TIGRPAMS; TIGR00166; S6; 1.
PROSITE; PS014049; RIBOSOMAL_S6; FALSE NEG.
Ribosomal protein; FRNA-binding; Complete proteome.
SEQUENCE 149 AA; 17274 NW; 1576686EEAEFFIRC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 BY SIMILARITY.
17302 MW, BD11C52CEB186033 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; L 100.0%; Pred. No. 1.7e+02;
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                                           entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacterium thermoautotrophicum.
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InterPro; IRPR002579; DUF25.
Prom; P001641; SelR; 1.
ProDom; P0004057; DUF25; 1.
TIGRFAMs; TIGR0357; TIGR0357; 1.
Oxidoreductase; Complete proteome.
ACT_SITE 136 136 BY SIMII
                                                                                                                                                                                       HAMAP; MF_00360; -; 1.
InterPro; IPR000529; Ribosomal_S6.
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PIR; A69195; A69195.
                                                                                                                                                EMBL; AL591786; CAC45717.1; -.
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Dolashka-Angelova P., Stevanovic S., Dolashki A., Angelova M., Serkedjieva J., Pashova S., Zacharieva S., Voelter W.; "Structural and functional analyses of glycosylated Cu/Zn-superoxide dismutase from the fungal strain Humicola lutea 103, cultivated in copper stress.; "Biol. Chem. 278:0-0(2003).
                                                                                                                                                 SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, MASS SPECTROMETRY AND GLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MASS SPECTROMETRY: WW=1593; METHOD=MALDI.
-!- MASS SPECTROMETRY: WW=1593; METHOD=MALDI.
-!- SIMILIARITY: Belongs to the Cu-Zn superoxide dismutase family.
InterPro; IPRO1424; SOU ZN.
Pfam; PF00080; Sodcu; 1.
PRO081; CUZNISMTASE.
PROD080; PRO0068; CUZNISMTASE.
PROSTIE; PS00087; SOU ZN, 1.
PROSTIE; PS00087; SOU ZN, 2; 1.
PROSTIE; PS00087; SOU CUZN, 2; 1.
  15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
Hunicola lutea.
Eukaryota, Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
NCBI_TaxID=253246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
83
120 1
57 1
23
152 AA;
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Best Local
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kininogen-1 precursor (BMK-1) [Contains: Maximakinin, Bradykinin].
Bombina maxima (Giatt fire-bellied toad) (Chinese red belly toad).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Archeobatrachia, Bombinatoridae, Bombina.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ315488; CAC48026.2; -.
Amplibian defense peptide; Vasodilator; Bradykinin; Repeat; Signal.
SIGNAL 23 KININOGEN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Skin secretion, and Venom gland;
MEDLINE-22830826; PubMed=12948837;
Chen T., Bjourson A.J., McClean S., Orr D.F., O'Kane E.J., Rao P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of maximakinin precursor cDNAs from Chinese toad, Bombina maxima, venom.";
                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides 24:853-861(2003).
-!- FUNCTION: Potent vasodilator. Binds B1 and B2 bradykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 1; Length 152; 100.0%; Pred. No. 1.7e+02; trive 0; Mismatches 0; Indels
100.0%; Score 25; DB 1; Length 151; 100.0%; Pred. No. 1.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., SEQUENCE OF MAXIMAKININ, AND SYNTHESIS MAXIMAKININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRADYKININ.
B58B31389D837686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- SIMILARITY: Belongs to the bradykinin family.
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BRADYKININ.
MAXIMAKININ.
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BRADYKININ.
MAXIMAKININ.
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SODC HUMLT STANDARD;
1
AC P836B4;
DT 15-MAR-2004 (Rel. 43, Created)
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17604 MW;
                 Best Local Similarity 100.
Matches 4; Conservative
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152 AA;
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es 4; Conserv
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                                                                                  1 GPRP 4
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Q90WB8;
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Query Match
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RNIL BOWMY
IN LANA BOWN
DT 15-MAR DEPTILE FT PEPTILE FT PETILE FT PET
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COPPER (BY SIMILARITY).
COPPER AND ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
COPPER (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                          h Score 25; DB 1; Length 152; Similarity 100.0%; Pred. No. 1.7e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                          N-LINKED (GLCNAC. . .).
4295345C2ADA1203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 31

RS6 AGRT5

AC RS6 AGRT5

STANDARD; PRT; 153 AA.

AC S04GE7;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 38-FEB-2003 (Rel. 41, Last annotation update)

DF 30S ribosomal protein S6.
                                                                                                                                                               23 N
15732 MW;
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Neurospora crassa.";
J. Biol. Chem. 260:9559-9566(1985).
-!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
-!- CATALYMIC ACTIVITY: 2 superoxide + 2 H(+) = 0(2) + H(2)0(2).
-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                            AEQUENCE FROM N.A.
MEDILINE=91035418; PubMed=2146266;
Chary P., Hallewell R.A., Natvig D.O.;
Chary tr., Hallewell R.A., and chromosome mapping of the gene for "Structure, exon pattern, and chromosome mapping of the gene for cytosolic copper-zinc superoxide dismutase (sod-1) from Neurospora
                                                    Eukaryota, Fungi, Ascomycota, Pezizomycotina; Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora,
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                         MEDLINE=85261356; PubMed=3160699;
Lerch K., Schenk E.;
"Primary structure of copper-zinc superoxide dismutase from
Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)
SOD-1.
                                                                                                                                                                                                                           assa.";
Biol. Chem. 265:18961-18967(1990).
                                              Neurospora crassa.
                                                                                                                                                                                                                       crassa."
                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Houndel K., Gordon J., Vandin M., Lartchouk O., Epp A., Liu F.,

Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

Genome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens CSB.",

Science 294:2232-2238(2011).

-!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                              MEDLINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S. Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                               Nester B.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SIMILARITY: Belongs to the S6P family of ribosomal proteins.
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         RPSF OR ATU1091 OR AGR C_2022.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR000529; Ribosomal_S6.
Pfam, PF01250; Ribosomal_S6; 1.
ProDom; P0003809; Ribosomal_S6; 1.
TIGRPAMS; TIGR00166; S6; 1.
PROSTIFE; PS01048; RIBOSOMAL_S6; FALSE NEG.
Ribosomal profein; RRNA-binding; Complete proteome.
SEQUENCE 153 AA; 17766 MW; 79C494057455977F CRC64;
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(Rel. 19, Last sequence update)
(Rel. 42, Last annotation update)
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PIR; AB2711; AB2711.
HAMAP; MF_00360; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000529; Ribosomal_S6.
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                                                                                                                                                                                                                                                                                                                                                                 Science 294:2317-2323(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=176299;
                                                                                                                   SEQUENCE FROM N.A.
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01-AUG-1991 (
10-OCT-2003 (
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P07509;
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SODC NEUCR
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Matches
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similarity)
-! SUBDIAT: Howodimer.
-! SUBCELLULAR LOCATION: Cytoplasmic.
-! SUBCELLULAR LOCATION: Cytoplasmic.
-! SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.
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COPPER (BY SIMILARITY).
COPPER AND ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS000469; SOD CU_ZN; I.
PROSITE; PS00087; SOD CU_ZN_1; I.
PROSITE; PS00332; SOD CU_ZN_2; I.
Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc. INIT MET 46 46 COPPER (BY SIMILARITY).
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BY SIMILARITY.

T -> A (IN REF. 2).

56DAFAC86CD9573B CRC64;
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ZINC (BY SIMILARITY)
ZINC (BY SIMILARITY)
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Pred. No. 1.7e+02;
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InterPro; IPR01424; SOD_CU_ZN.
Pfam; PF00080; sodcu; 1.
PRINTS; PR00068; CUZNIEMTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15753 MW;
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P00445;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomyces.
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Johansen J.T., Overballe-Petersen C., Martin B., Hasemann V.,
Svendsen I.;
                                                                                                   SEQUENCE FROM N.A.
MEDLINE=88263032; PubMed=3290902;
Bermingham-Mcdonogh O., Gralla E., Valentine J.;
The copper. zinc-superoxide dismutase gene of Saccharomyces cerevisiae: cloning, sequencing, and biological activity.";
Proc. Natl. Acad. Sci. U.S.A. 85:4789-4793(1988).
                                                                                                                                                                                                                                                                                                                                                                         STRAIN=X2180-1A;
Frutiger S., Hughes G.J., Sanchez J.-C., Hochstrasser D.F.;
Submitted (FBB-1996) to Swiss-Prot.
                                                                                                                                                                                    Ramezani Rad M., Kirchrath L., Hollenberg C.P.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
SUD-CYCHE dismutase [Cu-Zn] (EC 1.15.1.1).
SODI OR YOR104C OR J1968.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
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                                                                                   VCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                  R GO; GO:0005829; C:cytosol; IDA.

R GO; GO:0005758; C:mitochondrial intermembrane space; IDA.

R GO; GO:0006758; C:mitochondrial intermembrane space; IDA.

R GO; GO:0006801; E:copper; zinc superoxide dismutase activity; IDA.

R GO; GO:0006802; E:copper ion homeostasis; IGI.

R GO; GO:0006802; P:superoxide metabolism; IMP.

R O; GO:0006802; P:superoxide metabolism; IMP.

R InterPro; IPR001424; SOD_CU_ZN.

R PRINTS; PR00068; CUZNDISMTASE.

R PRODOM; PR0006459; SOD CU_ZN; 1.

R PROSITE; PS000087; SOD_CU_ZN 1; 1.

R PROSITE; PS000087; SOD_CU_ZN 1; 1.

R Anticiant; Oxidoreductase; Metal-binding; Copper; Zinc;
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15723 MW; 4B431A9B5D3211BE CRC64;
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                                                        EMBL, J03279; AAA34543.1; --
EMBL, Z49604; CAA89634.1; --
FIR, AA1114, DSBYC.
PDB, 1SDY, 31-JAV-94.
PDB, 1VSO; 10-JUN-96.
PDB, 1UCV; 08-MAR-96.
PDB, 1B4L, 23-DEC-99.
PDB, 1E19; 18-DEC-99.
PDB, 1F19; 18-DEC-02.
PDB, 1F19; 18-DEC-02.
PDB, 1F10; 18-DEC-02.
PDB, 1F10; 18-DEC-02.
PDB, 1F10; 18-DEC-02.
PDB, 1F10; 12-DEC-02.
PDB, 1F10; 12-DEC-02.
PDB, 1VAZ; 12-JAN-00.
GermOnline; 141937; VEAST.
SWISS-2DPAGE; PO0445; YEAST.
SGD; SGO03865; SODI.
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138
145
150
153 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete amino acid sequence of copper, zinc superoxide dismutase from Saccharomyces cerevisiae."; Carlsberg Res. Commun. 44:201-217(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=92126276; PubMed=1772629;
Dinovic K., Gatti G., Coda A., Antolini L., Pelosi G., Desideri A., Falconi M., Marmocchi F., Rotilio G., Bolognesi M.;
"Structure solution and molecular dynamics refinement of the yeast Cu. Zn enzyme superoxide dismutase.";
Acta Crystallogr. B 47:918-927(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92292161; PubMed=1602482;
Djinovic K., Gatti G., Coda A., Antolini L., Pelosi G., Desideri A., Falconi M., Marmocchi F., Rotilio G., Bolognesi M.;
"Crystal structure of yeast Cu, Zn superoxide dismutase.
Crystallographic refinement at 2.5-A resolution.";
J. Mol. Biol. 225:791-809(1992).
                                                                                                                                                                                                                                                                                                                                                                           Steinman H.M.;
"The amino acid sequence of copper-zinc superoxide dismutase from backers' yeast.";
J. Biol. Chem. 255:6758-6765(1980).
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157 AA; 17572 MW; 177C94B4EB066169 CRC64;
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131 GPRP 134
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Q00163;
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GTR4_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20365717; Pubmecal 109-10347;

RA SIMPROON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

Bueno M.R.P., Canacrosi E.D., Bordin S., Bove D.M., Brinnes M.R.S.,

RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Carrer H.,

Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Carrer D.M.,

RA Continho L.L., Cristofani M., Dias.Neto E. Docena C., El-Dorry H.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA P.L., Hoheisel J.D., Jungreira M.C., Gruber A.,

RA D.L., Hoheisel J.D., Jungreira M.E., Marchado J.R.,

Raciose J.S., Marchins E.B., Madeira H.M.F., Marchado J.R.,

Machado M.A., Madeira A.M.B., Madeira H.M.F., Marchado J.R.,

Machado M.A., Madeira A.M.B., Mattins E.M.F., Marshuma A.Y.,

RA Marchado M.V., Martins E.A.L., Martins E.M.F., Marshuma A.Y.,

RA Mani A.J., Nascimento A.L.T.O., Netto L.E.S.,

Mond D.H., Nobrega F.G., Nunes L.R., Oliveira M.A.,

RA Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

RA Oliveira M.C., de Silva A.M., da Silva F.R., Silva W.A. Jr.,

RA Silva A.C.R., da Silva R.M., da Silva F.R., Silva W.A. Jr.,

RA Salva A.C.R., da Silva R.M., da Silva F.R., Silva W.A. Jr.,

RA Zago M.A., Zatz M., Meddanis J., Setubal J.C.,

Nature 406:131-159(2000).

Hrus 406:131-159(2000).
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                        .
0
                       Length 153;
                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
N utilization substance protein B homolog (NusB protein).
                                                                      0; Indels
                    100.0%; Score 25; DB 1; I 100.0%; Pred. No. 1.7e+02; ive 0; Mismatches 0;
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HSSP; P04381; 1EY1.
HAMAP; MF 00073; -; 1.
InterPror; IPRO06027; NusB.
Franscription termination; Complete proteome.
                                                                                                                                                                                                                                                                                             157 AA.
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-!- SIMILARITY: Belongs to the nusB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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Query Match
Best Local Similarity 100.0
Loca 4; Conservative
                                                                                                                                                                                                                                                                                             STANDARD;
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Xylella fastidiosa.
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                                                                                                                       1 GPRP 4
                                                                                                                                                                                                                                                                                          XYLFA
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                                                                                                                                                                                                                                            RESULT 34
NUSB_XYLFA
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                                                              Gaps
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member (Glucose transporter type 4, insulin-responsive) (Fragment).
SLC244 OR GLUT4.
Canis familiaris (Dog).
Eukaryota; Metazoa; Ohordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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   Length 157;
100.0%; Score 25; DB 1; Length 15
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001841; Znf_ring.
SMART, SM00184, R.NG, 1.
Hypothetical protein; Zinc. Zinc.finger.
SEQUENCE 158 AA; 17082 MW; BCDE6BC474CEE75E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ictalurid herpesvirus I (Channel catfish virus) (CCV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Ictalurid Herpes-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davison A.J.; "Channel catfish virus: a new type of herpesvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical gene 9 zinc-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M75136; AAA88190.1; -. EMBL; M75136; AAA88112.1; -.
                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 186:9-14(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A36787; ZBBEI1.
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Best Local Similarity
                             Local Similarity
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                                                                                                                                  primarily to the perinuclear region, undergoing continued recycling to the plasma membrane where it is rapidly reinteringlized. The dileucine internalization motif is critical for intracellular sequestration (By similarity).

--- PTM: Sumoylated (By similarity).

--- SIMILARITY: BELONGY TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE TRANSPORTERS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
1 ransmembrane; Sugar transport; Transport; Multigene family.
NON_TER
                                                                                           MEDLINE=20422104; PubMed=10964405;
Pichon B., Mercan D., Poulllon V., Christophe-Hobertus C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
9 (POTENTIAL).
EXTRACELUTAR (POTENTIAL).
10 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AJ388533; CAB46835.1; -.
InterPro; IPR007114; MFS.
InterPro; IPR01828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005632; Sugar_transpt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005020; Sug_transport
InterPro; IPR005829; Sugar_transport
InterPro; IPR00363; Sugar_transp)
Pfam; PP00083; sugar_tr; 1.
   8 05:50:42 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0171; SUGRIRNS
PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
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162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GPRP 4
                                                                                                                          Christophe D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
NON TER
SEQUENCE
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TRANSMEM
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Wed Sep
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0
                                                                       100.0%; Score 25; DB 1; Length 162; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                      17453 MW; 0C58CBB23C6AD2BB CRC64;
CYTOPLASMIC (POTENTIAL).
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104 GPRP 107
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01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Chloroplast 30S ribosomal protein S18.
                    PRT;
                    STANDARD;
                                                                                             Oryza sativa (Rice).
                    ORYSA
                              P12152;
RESULT 37
RR18_ORYSA
                                                                                   RPS18.
                    RR18
                    OCCUPATO
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163 AA.

Chloroplast. Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

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                                                                                                                  Historical Minimada H., Whittler R., Ishibashi T., Sakamoto M., Mori M., Kondo C., Honji Y., Sun C.-R., Menga B.-Y., Li Y.-Q., Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.; Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura M.; The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals."; Mol. Gen. Genet. 217:185-194(1989).

-!- SUBUMIT: Part of the 30s Tibosomal subunit.
-!- SUBCILITAR LOCATION. Chloroplast.
-!- SIMILARITY: Belongs to the S18P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIN, JUGACHO, NO. CARAMERE, P. 12152; -...
HAMARP, MF 00270; -.; 1.
InterPro; IPR001648; Ribosomal S18.
PRIM: PR01084; Ribosomal S18; 1.
PRINTS; PR00974; RIBOSOMALS18; 1.
PRODOM; PD002239; Ribosomal S18; 1.
TIGREMMS; TIGR01165; S18; 1.
PROSITE; PS00057; RIBOSOMAL S18; 1.
PROSITE; PS00057; RIBOSOMAL S18; 1.
PROSITE; PS00057; RIBOSOMAL S18; 1.
PROSITE; PS00057; RAP-binding; Chloroplast; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (G-CSF-induced gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] --
SEQUENCE FROM N.A.
MEDLINE=93209815; PubMed=8458737;
Turman M.A., Yabe T., McSherry C., Bach F.H., Houchins J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 1; Length 163; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 AA; 19643 MW; 79DA5CB42C125DE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
protein NKO7 (Natural killer cell protein 7)
protein) (Protein GIG-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 AA
                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
MEDLINE=89364698; PubMed=2770692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X15901; CAA33970.1; -. PIR; JQ0248; R3RZ18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 GPRP 126
                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GPRP 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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REPEAT
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NKG7 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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POTENTIAL

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Homo sapiens
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TRANSMEM
TRANSMEM
TRANSMEM
                                                                         SEQUENCE
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FGFM HUMAN
                                                                                                                                                                         Matches
  87 FT S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAX Strausberg R.D., PubMed=12477932,

Ray Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Ray Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Ray Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ray Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ray Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

Ray Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Ray Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Ray Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Ray Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Morley M., Sodergren E.J., Lu X., Gibbs R.A.,

Ray Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rahes J., Schein J.E., Jones B.D., Dickson M.C.,

R. Rakesley R.W., Touchman J.W., Schwutz J., Myers R.M.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length

R. Tissub Specificity: Expressed in motive protein (Potential).

C. -- TISSUB SPECIFICITY: Expressed in brain, heart, or

skeletal muscle. Expressed in brain, heart, or

skeletal muscle. Expressed in some TCR alma deta-

clones (both CD4+ and CD8+), but me sort expressing CTL

clones (both CD4+ and CD8+), but is sont expressed in other TCR

alpha beta-expressing CTL clones and in cell lines representing B

c. -- SIMILARITY: Belongs to the PMP-22 / EMP / MP20 family.
                                                                                                                        MEDLINE=94168584; PubMed=7510105; Shimane M.; Tani K.; Maruyama K.; Tani K.; Maruyama K.; Takahashi S.; Ozawa K.; Asano S.; Molecular cloning and baracterization of G-CSF induced gene cDNA."; Biochem. Biophys. Res. Commun. 199:26-32(1994).
"Characterization of a novel gene (NKG7) on human chromosome 19 that is expressed in natural killer cells and T cells.";
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Church R.L., Li X.L., Wang J.H.;
"Human chromosome 19q13.4 DNA sequence, including complete sequence
for LIM2 and NKG7.";
                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 606008; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.
InterPro; IPR004031; PMP22_Claudin.
InterPro; IPR004032; PMP22_Claudin.
PF00822; PMP22_Claudin; I.
PF00822; PMP22_Claudin; I.
PROSITE; PS01221; PMP22_1; FALSE_NEG.
PROSITE; PS01222; PMP22_2; FALSE_NEG.
Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Blood;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF305941; AAG32329.1; -. EMBL; BC015759; AAH15759.1; -.
                                               Hum. Immunol. 36:34-40(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U09608; AAA18209.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, JC2081; JC2081.
Genew, HGNC:7830; NKG7.
                                                                              [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; Genome Res. 13:226-2270(2003).
-!- FUNCTION: May be involved in hair development.
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22887296; PubMed=12975309; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Clark H.F., Gurney A.L., Crowley C., Currell B., Douel B., Dowd P., Eaton D., Poster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewis D., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Fibroblast growth factor-22 precursor (FGF-22) (UNQ2500/FRO5800).
                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIANE=21240339; PubMed=11342227;
Nakatake Y., Hoshikawa M., Asaki T., Kassai Y., Itoh N.;
"Identification of a novel fibroblast growth factor, FGF-22,
preferentially expressed in the inner root sheath of the hair follicle.";
                                                                                                                                                         Length 165;
                                                                                                                          Score 25; DB 1; Lengtn 1v. Pred. No. 1.88+02;
                                                                                           CEE2901B6DC42A8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 605831; -.
GO; 6005615; C:extracellular space; NAS.
GO; GO:0030154; P:cell differentiation; NAS.
InterPro; IPR008996; Cytok ILI_like.
InterPro; IPR002348; ILI_HBGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 AA.
                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1517:460-463(2001).
                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB021925; BAB13479.1; -. EMBL; AY359084; AAQ89955.1; -.
                                                                                               17664 MW;
                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:3679; FGF22.
MIM; 605831; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
61
92
133
165 AA;
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        157 GPRP 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissum=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                          1 GPRP 4
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115
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                                                                                                                                                                                                                                                                                              24
83
131
                                                                                                                                                                                                                                                                                                                                                                                                               131
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168
82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT7 BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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PEPTIDE
PEPTIDE
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MOD_RES
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         DORRER THE TEST THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-WAR-2004 (Rel. 43, Last amoctation update)
15-WAR-2004 (Rel. 43, Last amoctation update)
Glucagon-family neuropetides precursor [Contains: Growth hormone-
releasing factor (GRF) (Growth hormone-releasing hormone) (GHRH);
Philutary adenylate cyclase activating polypeptide-27
(PACAP-27)
(PACAP-38) (PACAP38)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCRORY J.E., Parker R.L., Sherwood N.M.,
"Expression and alternative processing of a chicken gene encoding
the processing of a chicken gene encoding
both growth hormone-releasing hormone and pituitary adenylate
cyclase-activating polypeptide.";
DNA Cell Biol. 16:95-102(1997).
                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; Length 170; 100.0%; Pred. No. 1.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                      FIBROBLAST GROWTH FACTOR-22.
CB88918C2D5A4CE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3; Name=GRF 1-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the glucagon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=GRF 1-43;
IsoId=P41534-2; Sequence=VSP_001760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P41534-3; Sequence=VSP_001759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P41534-1; Sequence=Displayed;
                                                                                                                                                                             POTENTIAL.
Pfam; PF00167; FGF; 1.
PRINTS, PR00262; 1L1HBGF.
PRODOM; PR000831; IL1 HBGF; 1.
SMART; SM00442; FGF; 1.
PROSTIE; PS00247; HBGF FGF; FALSE_NEG.
Growth factor; Signal.
22
GRONL
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SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97174314; PubMed=9022048;
                                                                                                                                                                                                                                    SEQUENCE 170 AA; 19662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U71183; AAB51200.1; -.
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                      170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 GPRP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                         1 GPRP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PACA CHICK
AC DID PACA CHICK
AC 115-UUL-1998
DT 15-UUL-1998
DT 15-UUL-1998
DE Glucagon-frat
DE FILUITATY ad
DE FILUITATY ad
DE (PACAP-39) (
GN GAILUS GAILUS
CO BUKATYOLA; P
CO BUKATYOLA; P
CO BUKATYOLA; P
CO BUKATYOLA; P
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CO BUKATYOLA; P
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EMBL; U71184; AAB51201.1; -.
EMBL; U71185; AAB51202.1; -.
InterPro; IPR000532; Glucagon.
Pfam; PF00123; hormone2; 2.
PRINTS; PR00255; GLUCAGON.
SMARY; SM00070; GLUCAGON.
SMARY; SM00070; GLUCAGON; 2.
PROSITE; PS00260; GLUCAGON; 2.
Anidation; Alternative splicing.
Anidation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frank R.W., Gennaro R., Schneider K., Przybylski M., Romeo D.; "Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of bovine neutrophils."; "Brol. Chem. 265:18871-18874(1990).
                                                                                                                                                                                                                                                                                  GROWTH HORMONE-RELEASING FACTOR 1-46. PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE-38.
                                                                                                                                                                                                                                                                                                                                                       PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPERTIDE—27 AMIDATION (G-158 PROVIDE AMIDE GROUP).
AMIDATION (G-169 PROVIDE AMIDE GROUP). RHADGIFSKAYRKLIGOLSARNYLHSIMAKRVG -> S (in isoform GRF 33-46).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 1; Length 175; Similarity 100.0%; Pred. No. 1.9e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform GRF 1-43) /FIId=VSP_001760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Bone marrow;
MEDLINE=95010707; PubMed=7925973;
Scocchi M., Romeo D., Zanetti M.;
"Molecular cloning of Bac7, a proline- and arginine-rich antimicrobial peptide from bovine neutrophils.";
FEBS Lett. 352:197-200(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zanetti M.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ODB54995F0AA9DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bactenecin 7 precursor (BAC7) (PR-59).
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Storici P., Tossi A., Lenarcic B., Romeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91035404; PubMed=2229048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 AA; 19560 MW;
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                                                                                                                                                                                                                                       23
80
128
168
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168
114
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Submitted (DEC-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [3]
SEQUENCE OF 131-189.
TISSUE=Neutrophils;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Dyn. 218:102-111(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                             Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 GPRP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          critical region."
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     DDT TOD DDT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                         cathelicidins, precursors of antimicrobial peptides.";

Eur. J. Blochem. 238:769-776(1996).

-!- FUNCTION: Exerts, in vitro, a portent antimicrobial activity.

Probably due to an impairment of the function of the respiratory chain and of energy-dependent activities in the inner membrane of susceptible microorganisms.

-!- TISSUE SPECIFICITY: Large granules of neutrophils.

-!- PTM: Blastase is responsible for its maturation.

-!- PTM: Blastase is responsible for its maturation.

-!- MASS SPECTROMETRY: WW=18395; WW_ERR=1; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APIO_ARATH STANDARD; PRT; 192 AA.
Q9ZPWZ; QBLBLB;
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
10-OCT-2009 (Rel. 42, Last annocation update)
Anaphase promoting complex subunit 10 (APC10) (Cyclosome subunit 10)
Anaphase promoting complex subunit 10 (APC10) Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-CV. Columbia,
MEDLINE-20083487; PubMed=10617197;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronlin L.A., Shen M., Pail G., Van Aken S., Umayam L.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Mierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMEL, Y09471; CAA70010.1., ...
InterPro; IPR001894; Cathelicidin.
Fran, Pr00666; Cathelicidins; 1.
ProDom; PD001889; CATHELICIDINS, 1.
PROSITE; PS00946; CATHELICIDINS, 1; 1.
PROSITE; PS00947; CATHELICIDINS, 2; 1.
Antibiotic; Repeat; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 1; Length 19
100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130
190
EACTENBECIN 7.
190
EXEMOVED PARTIALLY.
30
PYRROLIDONE CARBOXYLIC ACID.
96
124
124
3, 21567 MW, 8CD07D7AA30A731C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID
       "Purification and structural characterization of bovine
                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L42977; AAA87359.1; -. EMBL; Y09471; CAA70616.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 ĠPRP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD RES
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE
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Matches
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                                                                                                                     "Full-length cDNA from Arabidopsis thaliana.";
"Full-length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Component of the anaphase promoting complex/cyclosome (APC/C), a cell cycle-regulated ubiquitin ligase that controls progression through mitosis and the G1 phase of the cell cycle (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CD-1; TISSUE=Embryo;
MEDLINE=20284895; PubMed=10822263;
Galili N., Nayak S., Epstein J.A., Buck C.A.;
"Raf4, a RING protein expressed in the developing nervous and
reproductive systems, interacts with Gscl, a gene within the Dideorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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SEQUENCE FROM N.A.

MEDLINE-21085660; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                eimilarity).
-!- SUBONIT: The APC is composed of at least 11 subunits (By
similarity).
-!- SIMILARITY: Belongs to the APC10 family.
SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Figure for solution pathway; Cell cycle; Mitosis.

CONFLICT 112 112 E -> D (IN REF. 2).

SEQUENCE 192 AA; 21750 MW; 5ADBEOE8F7D12FFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 1; L
100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNF4 MOUSE STANDARD; PRT; 194 AA. Q9QSS2; 035941; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) RING finger protein 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC006439; AAD15507.2; -. EMBL; AY087130; AAM64688.1; -. Interpro; IPR004939; APC10. Pfam; PF03256; APC10; 1.
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Gaps

0,

0; Indels

TISSUE=Embryo; MEDLINE=98140125; PubMed=9479498; SEQUENCE OF 16-178 FROM N.A. [5] INTERACTION WITH TCF20. SEQUENCE FROM N.A. Hayashizaki Y.;

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  MGD; MGI:1201691; KILL.
INTERPRO; IPR001841; Znf ring.
Pfam; PF001097; Zf-C3HC4; I.
PFAM; SM00184; RING; I.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS0089; ZF RING 2; 1.
TRANSCIPCION regulation; Activator; Zinc-finger; Nuclear protein.
Transcription regulation; RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 1; I
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Scc...
v 100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIŜSUE-Retina;
MEDLINE-96213684; PubMed-8647247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96279248; PubMed=8663313;
                                                                                                          EMBL; AF169300; AAF00620.1; --
EMBL; AK01917; BAB31585.1; --
EMBL; BC032282; AAH03282.1; --
EMBL; U95141; AAC53539.1; --
MGD; MGI:1201691; Rnf4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosomal localisation.";
FEBS Lett. 385:185-188(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q16774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE=22388257; PubMed=12477932;

Warausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Butchew K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Batchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Abatchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Phesy J., Helton E., Ketteman M., Madrid A.R., Gibbs R.A.,

Phesy J., Helton E., Ketteman M., Maching M., Rodrigues S., Sanchez A.,

Huiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalsku U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalsku U., Smailus D.E.,

Chimerod J., Schmutz J., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length

Phyc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuchl P., Lewis S., Matsuc Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-!- TISSUE SPECIFICITY: In the embryo, expressed primarily in the developing nervous system with strong expression in the dorsal root ganglia and gonads. Ubiquitously expressed in the adult.
-!- DEVELOPMENTAL STAGE: Expression is detected from embryonic day 7 and continues throughout development and into adulthood.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20408957; PubMed=10849425; Lyngsoe C., Bouteiller G., Damgaard C.K., Ryom D., Sanchez-Munoz S., Noerby P.L., Bonven B.J., Josegensen P.; Interaction between the transcription factor SPBP and the positive cofactor RNF4. An interplay between protein binding zinc fingers."; J. Blol. Chem. 275:26144-26149 (2000).

-1- FUNCTION: Enhances steroid teceptor-mediated transcriptional activation as well as activating basal transcription (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SUBUNIT: Interacts with GSCL, Androgen receptor, TCF20, TBP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chiariotti L., Benrouto G., Fedele M., Santoro M., Simeone A., Fusco A., Bruni C.B., "Identification and characterization of a novel RING-finger gene (RNR4) mapping at 4016.3."; Genomics 47:258-265(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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A REDINES_2388257; PubMed=12477932;

X MEDLINES_2388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fitzgibbon J., Katsanis N., Wells D., Delhanty J., Vallins W., Hunt D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human guanylate kinase (GUK1): cDNA sequence, expression and
                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Guanylate kinase (EC 2.7.4.8) (GMP kinase).
196 AA
    HID DATA BERKER BERKER
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                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P15454; IGKY.

RILLE-PPO; IPR008144; Guanylate kin.

RILLE-PPO; IPR008145; Guanylate kin.

REAM; PP00625; Guanylate kin; 1.

REAM; SM0072; GuKc; 1.

REAM; SM0072; GuKc; 1.

REAM; PS00856; GUANYLATE KINASE 1; 1.

RECSITE; PS00856; GUANYLATE KINASE 2; 1.

RECSITE PS00856; GUANYLATE KINASE 1; 1.

RECSITE PS00856; GU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
-!- CATALYTIC ACTIVITY: ATP + GMP = ADP + GDP.
-!- SUBUNIT: Monomer (By similarity).
-!- SIMILARITY: Belongs to the guanylate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Lk
100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Guanylate kinase (EC 2.7.4.8) (GMP kinase).
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PDB, 1LVG, 1L-DEC-02.
MGD; MG1:95811; Gukl.
InterPro; IPR008144; Guanylate_kin.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; X67029; CAA47423.1; -. PIR; S39447; S39447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||
2 GPRP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUK1 OR GMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGUA MOUSE
Q64520;
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         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=94271265, PubMed=7911663;
Gaidarov I.O., Suslov O.N., Ovchinnikova T.V., Abdulaev N.G.;
Guanylate kinase from bovine retina: isolation, primary structure,
and expression in 0.01,",
Bioorg. Khim. 20:367-381(1994).
-!- FUNCTION: Essential for recycling GMP and indirectly, cGMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                               human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Essential for recycling GMP and indirectly, cGMP.

-!- CATALYITC ACTIVITY: ATP + dFMP + GDP.

-!- SUBUNIT: Monomer (By similarity).

-!- SUBUNITY: Belongs to the guanylate kinase family.
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INIT_MET 0 BY SIMILARITY.

MDF EIND 10 TATP (BY SIMILARITY).

MOD RES 1 ACETYLATION (BY SIMILARITY).

SEOÜENCE 196 AA; 21594 MW; C4727A7E2AA261B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 1; Length 19
100.0%; Pred. No. 2.2e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 139270; ---
GO; GO:0004385; F:guanylate kinase activity; TAS.
GO; GO:0006183; P:GTP biosynthesis; TAS.
InterPro; IPR008144; Guanylate kin.
InterPro; IPR008145; Guanylt/Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanylate kinase (EC 2.7.4.8) (GMP kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 AA
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SMART; SM00072; GuKC; 1.
PROSITE; PS00856; GUANYLATE KINASE 1; 1.
PROSITE; PS0052; GUANYLATE KINASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U66895; AAC50659.1; --
EMBL, BC006249; AAH06249.1; --
EMBL, BC009914, AAH06914.1; --
PIR; S68864; S68864.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:4693; GUK1.
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P46195;
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             SOTT THE SOURCE COURSE SERVING SOURCE COURSE SERVING SOURCE COURSE SOURC
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                                                                                                                                                                                                                                                            MEDLINE-96279248; PubMed-8663313;
Brady W.A., Kokoris M.S., Fitzgibbon M., Black M.E.;
"Cloning, characterization, and modeling of mouse and human guanylate
Kinases.";
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 271:16734-16740(1996).
-!- FUNCTION: Essential for recycling GMP and indirectly, cGMP.
-!- CATALYTICA ACTIVITY: ATP. + GMP = ADP + GDP.
-!- SUBDNIT: Monomer (By similarity).
-!- SIMILARITY: Belongs to the guanylate kinase family.
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RESULT 48
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI)
ARHGDIB OR GDID4.
Bos taurus (Boxina).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
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InterPro; IPR008145; Guanylt/Ca.
Pfam; PF00625; Guanyltate_Kin; 1.
PR051TE; PS00856; GUANYLATE_KINASE_1; 1.
PROSITE; PS0052; GUANYLATE_KINASE_2; 1.
Transferase; Kinase; AFP-binding; Actylation; 3D-structure.
INIT_MET 0 0 BY SIMILARITY.
NP_BIND 10 17 AAPP (BY SIMILARITY).
SEQÜENCE 197 AA; 21787 MW; 332403BF0DICCFB2 CRC64;
                                                                                                                                                  Similarity 100.0%; Score 25; DB 1; Length 197; Similarity 100.0%; Pred. No. 2.2e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 1; Length 200; 100.0%; Pred. No. 2.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTPase activation.
SEQUENCE 200 Aa; 22794 MW; EE8F1E38993AFDE5 CRC64;
                                                                                                                                                                                                                                                                                                           PRT; 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF182001; AAF00938.1; -. HSSP; P52566; 1DS6. InterPro; IPR007110; Ig-like. InterPro; IPR000406; Rho GDI. Pfam; PF02115; Rho GDI; I. PRINTS; PR00492; RHOGDI.
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Best Local Similarity 100...
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Q9TU03;
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GDIS BOVIN
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146 GPRP 149

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187 1
201 AA;
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Battow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Maxusina R., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Maxusina R., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Nilalon D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whitling M., Madan A., Coung A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI).
ARHGDIB OR GDID4.
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE=94085490; PubMed=8262133;
Leffers H., Nielsen M.S., Andersen A.H., Honore B., Madsen P.,
Vandekerckhove J., Celis J.E.;
"Identification of two human Rho GDP dissociation inhibitor proteins
whose overexpression leads to disruption of the actin cytoskeleton.";
Exp. Cell Res. 209:165-174(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "CDNA cloning of a human mRNA preferentially expressed in hematopietic cells and with homology to a GPP-dissociation inhibitor for the rho GTP-binding proteins."; Proc. Natl. Acad. Sci. U.S.A. 90:1479-1463(1993).
                                                Gaps
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUB-Brain;
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
"cDNA clones of human proteins involved in signal transduction sequenced by the Gulbrie cDNA resource center (www.cdna.org).";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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"Ly-CDI, a GDP-dissociation inhibitor of the RhoA GTP-binding protein, is expressed preferentially in lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 90:7568-7572(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93165719; PubMed=8434008;
Lelias J.M., Adra C.N., Wulf G.M., Guillemot J.C., Caput D.,
                        Length 200;
                       100.0%; Score 25; DB 1; Length 20
100.0%; Pred. No. 2.2e+02;
iive 0; Mismatches 0; Indels
22851 MW; EA78C965F1AB6F5C CRC64;
                                                                                                                                                                 201 AA.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-93361488; PubMed=8356058;
                                                Conservative
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                       Homo sapiens (Human)
200 AA;
                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                  146 GPRP 149
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                                                                          1 GPRP 4
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SEQUENCE
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                                                Matches
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Search completed: September 7, 2004, 18:58:47 Job time: 26 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES—M. tuberculosis; STRAIN=H37Rv;
MEDLINE=98295987; PubMed=95634330;
MEDLINE=98295987; PubMed=95634330;
A. Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Backock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gencles S., Hamlin N., Holroyd S., A Hornsby T., Jagels K., Kroch A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
In Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22709107, PubMed=12788972;
MEDLINE=22709107, PubMed=12788972;
Garnier T., Eiglineler K., Camus J.-C., Medina N., Mansoox H.,
Garnier T., Eiglineler K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. US.-A. 100:7877-7882(2003).
                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
Query Match 100.0%; Score 25; DB 1; Length 201; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, 273966; CAA98198.1; ALT_INIT.
EMBL, BX248341; CAD96966.1; -.
Tuberculist; Rv2086; -.
Hypothetical protein; Complete proteome.
SEQUENCE 201 AA; 22518 MW; 22AEC2268708FESB CRC64;
                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Very hypothetical protein Rv2086/Wb2113.
MyCobacterium tuberculosis, and
Mycobacterium boyis.
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SEQUENCE FROM N.A.
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YK86 MYCTU
ID YK86 MYCTU
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

September 7, 2004, 18:52:52; Search time 115 Seconds (without alignments) 10.975 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-931-009A-2 25 1 GPRP 4 Title: Perfect score: Seguence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65 summaries

SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
5: sp_human:*
6: sp_mammal:*
7: sp_mammal:*
8: sp_organelle:*
9: sp_bhage:* sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* sp_vertebrate:* sp_plant:*
sp_rodent:*
sp_virus:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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No.	Score	Match	Match Length DB	DB	ID	Description
; ; , 	25	100.0	27	11	Q99KX5	Q99kx5 musculu
7	25	100.0	31	4	Q9BVY4	Q9bvy4 homo sapien
m	25	100.0	36	12	Q91CY3	Q91cy3 tt virus. o
4	23	100.0	43	7	Q9EYJ2	Q9eyj2 streptococc
Ŋ	25	100.0	44	4	Q8TCB9	Q8tcb9 homo sapien
9	25	100.0	50	10	Q7X128	Q7xi28 oryza sativ
7	25	100.0	51	12	QSQPT9	Q8qpt9 tomato chlo
80	25	100.0	52	4	65unx8	Q9unx8 homo sapien
σ	25	100.0	53	ហ	Q9V8Y1	Q9v8y1 drosophila
10	25	100.0	26	11	9 0 S 260	Q9csg6 mus musculu
11	25	100.0	56	15	085655	Q85655 murine leuk
12	25	100.0	57	11	061460	Q61460 mus musculu
13	25	100.0	57	16	Q8VKP1	Q8vkp1 mycobacteri
14	25	100.0	65	ហ	Q9W3Q8	Q9w3q8 drosophila
15	25	100.0	99	'n	Q18234	Q18234 caenorhabdi
16	25	100.0	67	m	990868	Ogusé8 schizosacch

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ALIGNMENTS

Q99KX5 PRELIMINARY; PRT; 27 AA.
Q99KX5;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Mus musculus (Mouse).
Mus macany Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MOSE_TAXID=10090; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ER0039668, AAH03968.1; -. Hypothetical protein. SEQUENCE 27 AA; 2832 MW; 4008F368AF866B63 CRC64; SEQUENCE FROM N.A. RESULT 1 Q99KX5

Q9BVY4

RESULT 2

29BVY4

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
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                                                                                                                                                                                                                                                                                                                                                                                                                     Provencher C., Sirois S., Lapointe G., Roy D.;
Provencher C., Sirois S., Lapointe G., Roy D.;
Provencher C., Sirois S., Lapointe G., Roy D.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF321231; AAG38624.1; -
GO, GO:0016740; F:transferase activity; IEA.
InterPro; IPR003362; Bact transf.
Pfam; PF02397; Bact transf.
Transferase.
                                                                                                                                                                                                                                             Streptococcus thermophilus.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-20395; AAH22395.1; -..
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
43 43
43 AA, 4875 MW; 85DD21E6A95BA5DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8TCB9 PRELIMINARY; PRT; 44 AA.
Q8TCB9.
Q01CB9.
Q1-UNN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                   Last sequence update)
Last annotation update)
                                                             43 AA.
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                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequenc
01-JUN-2003 (TrEMBLrel. 24, Last annotat
Priming glycosyltransferase (Fragment)
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Q7X128;
01-OCT-2003 (TrEMBLrel 25, Created)
                                                             PRT;
                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1308;
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NON_TER
SEQUENCE
                                                                Q9EYJ2
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Q7XI28
   RESULT 4
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                                   Q9EYJ2
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                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Virology 288:358-368(2001).
EMBL; AB060599; BAB69922.1; -.
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0
Query Match 100.0%; Score 25; DB 11; Length 27; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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MEDLINE=21488921; PubMed=11601907;
Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
Yoshikawa A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 25; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC000821; AAH00821.1; -.
Hypothetical protein.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 31 AA; 3570 MW; E501FCF1DC4CB889 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 AA; 3878 MW; 875464E84E3A2A69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
ORFI (Fragment).
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Viruses, ssDNA viruses, Circoviridae, Anellovirus.
NCBI_TaxID=68887;
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                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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TISSUE=Placenta;
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                                                                                                                          1 GPRP 4
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091CY3

RESULT 3

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291CY3

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MEDLINE=99156873; PubMed=10037683; MEDLINE=99156873; PubMed=10037683; Sueyoshi T., Kawamoto T., Zelko I., Honkakoski P., Negishi M.; Sueyoshi T., Kawamoto T., Zelko I., Honkakoski P., Negishi M.; The repressed muclear receptor CAR responds to phenobarbital in activating the human CYP286 gene."; D. Biol. Chem. 274:6043-6046(1999).

EMBL, AF081569; AAD25243.1; -.

GO, GO:0006118; P:electron transport; IEA.

INTERPEO, IPROBLI28; Cyrochrome_P450.

NON TER
52
SEQÜENCE 52 AA; 5846 MW; 67933CB4DC69B76E CRC64;
                                                                                                                                                             Ouery Match
Best Local Similarity 100...
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  NCBI_TaxID=9606
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Ribeiro S.G., Ambrozevicius L.P., de Avila A.C., Calegario R.F.,
Ribeiro S.G., Lima M.F., Mello R.N., Rocha H., Zerbini F.M.;
"Distribution and genetic diversity of tomato-infecting geminiviruses in Brazil.",
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY049209; AAL82815.1; --
NON_TER 51
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                   Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                     STRAIN=CV. Nipponbare;
Sasaki T., Matsumcto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 12; Length 51; 100.0%; Pred. No. 4.1e+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  100.0%; Score 25; DB 10; Length 50; 100.0%; Pred. No. 4e+02; Ative 0; Mismatches 0; Indels
                                                                                                                                                          clone:POSOGCO7.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP004384, BAC79929.1;
Hypothetical protein.
SEQUENCE 50 AA; 5492 MW; B13E993B842B80DF CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome P450 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Capsid protein (Fragment).
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pypothetical protein P0506C07.3.
P0506C07.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomato chlorotic mottle virus.
Viruses; ssDNA viruses; Geminiviridae; Begomovirus
VCBI_TaxID=172391;
                                                                                                                                                                                                                       Query Match
Best Local Similarity 100...
4, Conservative
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Best Local Similarity 100...
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                                                                                                           SEQUENCE FROM N.A
                                                                                     NCBI_TaxID=39947;
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09UNXAC
09UN AC
09UN DT
01-M
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01-M
CYP20
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Gaps

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100.0%; Score 25; DB 4; Length 52; 100.0%; Pred. No. 4.2e+02; ative 0; Mismatches 0; Indels

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

REDINE=2019600; PubMed=10731132;

RA Amanatides P.G., Scherer S.E., Holf, H., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Holf, H., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Hichards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Man K.H., Doyle C., Baxendell M.D., Shango C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkorh C., Baldwin D.,

RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Bolcher A., Danlke C., Davenport U.B., Davies P.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Berman B.Y., Bhandari D., Dew I., Dietz S.M.,

Bockova D., Deloher A., Danlke C., Pavenport U.B., Davies P.,

RA Porler C., Gabrielian A.E., Garra N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houst D. L.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Morbherson D.,

RA Harris N., Moy M., Murphy B., Murphy L., Muzry D.M., Nelson D.L.,

RA Helson D.R., Nelson K.A., Li J., Li Z., Liang Y., Lin X.,

RA Helson D.R., Now M., Murphy B., Murphy L., Muzry D.M., Nelson D.R.,

Rainert K., Remington K., Sanders R., Pollard J., Puller S., Shen H.,

Spier E., Spradling A.C., Stapleton M., Strong R., Shith T.,

Shierskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RAMBOR D.A., Wang R., Weinstock G.M., Weissenbach J.,

Sylicskas R., Fetcor C., Turner R., Weinston B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                               09V8Y1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
CG15126 protein.
                                                                                                                                                                                                                                               PRELIMINARY;
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33 GPRP 36
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MEDLINE=91146586; PubMed=1997326;
Lakso M., Masaki R., Noshiro M., Negishi M.;
Lakso M., Masaki R., Noshiro M., Negishi M.;
Structures and characterization of sex specific mouse cytochrome P-
"Structures as members within a large family. Duplication boundary and
evolution.";
Eur. J. Biochem. 195:477-486(1991).
Eur. J. Biochem. 195:477-486(1991).
EMBL; M60359; AAA03650.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Duplan MuLV;
MEDLINE=89181946; PubMed=2538760;
Aziz D.C., Jolicoeur P., Zaher H.;
"Severe immunodeficiency disease induced by a defective Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                       Gag plo protein.

Murine leukemia virus.

Viruses, Retroid viruses, Retroviridae, Gammaretrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6387 MW; 4C2C72DFCC12FBA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Testosterone 16a-hydroxylase type c (Fragment).
CYP2B13 OR 16AOH-C.
                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukemia Virus.;
Nature 338:505-508(1989).
EMBL, X44576, CAA32719-1;
GO, GO:0019012; C:virion; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPRO01878; Znf CCHC.
Pfam; PF00098; Zf-CCHC, I.
PRINTS; PR00939; C2HCZNFINGER.
SWART; SM00343; Znf CCHC; I.
PROSITE; PS50158; ZF CCHC; I.
Core protein; Polyprotein.
SEQUENCE 56 AA; 6387 MW; 4C2C72DFCC12FBA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:88599; Cyp2bl3.

GO; GO:0004497; F:monooxygenase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR001128; Cytochrome_P450.

Pfam; PF00067; p450; 1.
                                                                                                                                                                                                        Created)
                                                                                                                                                               PRT;
                                                                                                                                                                                Q85655;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I49627
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 GPRP 51
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       1 GPRP 4
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Q61460;
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Q85655
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REALINE-57BL/66). PubMed-1217851;

REALINE-57BL/66). PubMed-1217851;

RAWAI J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Pubkunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aisawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,

RA Aisarto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RA Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner I., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Schriml L.M., Boffelli D., Bolinga N., Carninol P., & Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Mynshaw-Boris A., Yoshida K., Haesgawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,
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Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C., The genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000).

EMBL, AE003795; AAF57523.1; -.

FIYBase, FBGN0040729; CG15126.
SEQUENCE 53 AA, 5388 MW, 68828750C9C82142 CRC64;
                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Functional annotation of a full-length mouse cDNA collection.";
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Similarity 100.0%; Score 25; DB 11; Length 56;
4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                           100.0%; Score 25; DB 5; Length 53; 100.0%; Pred. No. 4.2e+02; ive 0; Mismatches 0; Indels
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:00056515; F:protein binding; IPI.
GO; GO:0004672; F:protein kinase activity; IDA.
GO; GO:0007165; P:signal transduction; IDA.
Pfam; FF00069; pkinase; I.
ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AA
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                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conservat
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Matches 4; Conserv
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Abril C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril V.P., Agbayani A., An H.-J., Andraws Pfannkoch C., Baldwin D., RA Ballaw R.M., Basu A., Baxendlad J., Bayraktaroglu L., Beaslay E.M., RA Ballaw R.W., Basu A., Baxendlad J., Bayraktaroglu L., Beaslay E.M., RA Berson K.Y., Bernan B.P., Bhandari D., Bolshakov S.P., RA Borkova D., Botchan W., Bouck J. Davles C., Davenport L.B., Davles P., Charry D., Canley S., Dahlke C., Davenport L.B., Davles P., Dietz S.M., RA Gerby D. B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fletschmann W., Roschen K., Gonger J. Garg N.S., Gelbart W.M., Glasser K., Andrews D., Heinan T.J., Wei M.-H., Ibegwam C., Harvey D. Heinan T.J., Wei M.-H., Ibegwam C., Harvey D. Heinan T.J., Wei M.-H., Ibegwam C., Lasko F., Karpen G.H., Re Z., Kenlison J.A., Kaecchum K.A., Harvey D., Heinan T.J., Wei M.-H., Ibegwam C., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Alalin M. Willen B.E., McIntosh T.C., McLedd M.P., McDreison D., Ra Martei B., McIntosh T.C., McLedd M.P., McDreison D., Martei B., McIntosh T.C., McLedd M.P., McDreison D., Martei B., McIntosh T.C., McJord M.P., Morskern D.R., Masser M., My W., Murphy B., Mursher W.P., Paris M. Martei B., McIntosh T.C., Scheeler F., Schen H., Ranger R., Spradling A.C., Standers R.D., Chinas S.M., My M., Murphy B., Mursher M.P., Smith T., Ranger B., Spradling A.C., Standers R.D., McHaller F., Sander H., Rang Z.-Y., Wassarman D.A., Wender M., Wang X., Mang Z.-Y., Wassarman D.A., Wender W., Zhou W., Zhou S., Zhu K., Zhang S., Zho Q., Zhao G., Zhanger E.W., Rubin G.M., Wenter J.C.; Zhanger E.W., Sunter J.C.; Zhanger S., Zhu W., Zhou X., Zhu X., Zhu W., Zhu W., Zhu 
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Ernokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 5; Length 65; 100.0%; Pred. No. 5.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 AA; 6385 MW; B9035B7A5BAC0F7C CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein C26F1.10.
C26F1.10.
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EMBL, AX103419; AAAF462624.1; --
EMBL, SY113619; AAM26624.1; --
Flybase; FBGN0040923; CG11368.
SEQUENCE 65 AA; 6385 MW: R90
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Best Local Similarity 100.
Matches 4; Conservative
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Q18234
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STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                   Gaps
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MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishai W.; "Mhole genome comparison of Mycobacterium tuberculosis clinical and
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Drosophila melanogaster (Fruit fly),
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Endopterygota, Diptera, Brachycera, Muscomorpha,
Bohydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                  100.0%; Score 25; DB 11; Length 57; 100.0%; Pred. No. 4.5e+02; Live 0; Mismatches 0; Indels
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100.0%; Score 25; DB 16; Length 57;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006936; AAK44510.1; -.
         Heme; Monooxygenase; Oxidoreductase.
NON TER 57 57
SEQÜENCE 57 AA; 6311 MW; 3FF9AA1979283DB9 CRC64;
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TOTAL MYDOCHELICAL Drotein.
HYDOCHELICAL S7 AA; 6035 MW; BBCA0B080B62690A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein MT0290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAX-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CG11368 protein (RH67809p).
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                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              33 GPRP 36
                                                                                                                                                                                                                                                       1 GPRP 4
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C08VKP1
AC C08VKP
DT 01-MP
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EMBL, AB028010; BAR87314.1, -.
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=968 h90;
MEDLINE=20223868; PubMed=10759889;
Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
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                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h Similarity 100.0%; Score 25; DB 3; Length 67; Similarity 100.0%; Pred. No. 5.3e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                     Length 66;
                                                                                                                                                                                                                                                        0; Indels
                                                                                                                       [3]
SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Materston R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U53148; AAB37072.2; -
PIR; T15646; T15646.
WormPep; C26FI.10; CE30733.
Hypothetical protein.
SEQUENCE 66 AA; 7486 MW; 8D2065216CB30F9F CRC64;
                                                           [2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Geisel C., Stellyes L., Bradshaw H.;
The sequence of C. elegans cosmid C26Fl.";
Submitted (APR-1996) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 67
67 AA; 7580 MW; DBD818EF169DF280 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                   Query Match
100.0%; Score 25; DB 5; I
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                            O9US68;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-UUN-2003 (TrEMBLrel. 24, Last annotati
Hypothetical nuclear protein (Fragment).
SPBC887.03C.
                                                                                                                                                                                                                                                                                                                                                  PRT;
  STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                               59 GPRP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
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                      Waterston R.;
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NON TER
SEQUENCE
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Q9US68
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Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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GO; GO:000682; F:protein kinase GK2 activity; IEA.
GO; GO:0004682; F:protein kinase CK2 activity; IEA.
GO; GO:0004674; F:protein kinase Historianse activity; IEA.
GO; GO:0007474; F:protein serine/threonine kinase activity; IEA.
GO; GO:0007219; P:intracellular signaling cascade; IEA.
InterPro; IPR002219; DAG PE-bind; IPA.
PFONISO; DAG PE-bind; 1.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Jaeckle H., de Almeida J.C., Galler R., Kluding H., Lehrach H.,
Edstroem J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                Balbiani ring 2 (BR2) gene (Fragment).
Chironomus pallidivittatus (Midge).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Chironomoldea;
Chironomidae; Chironominae; Chironomus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 11; Length 67; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 100.0%; Score 25; DB 5; Length 67 Local Similarity 100.0%; Pred. No. 5.3e+02; les 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; X65720; CAA46636.1; -.
HSSP; P28867; 1PTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edstroem J.E.;
Submitted (NOV-1985) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 AA; 7430 MW; D507C0FE873984FC CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
protein kinase (EC 2.7.1.37) (Fragment).
                             Last sequence update)
Last annotation update)
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PROSITE; PSSOO81; DĀG PE_BIND_DOM_2; 1.
Kinase; Transferase.
67 67
SEQŪENCE 67 AA; 7335 MW; 266A16372A
     Created)
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                            NCBI_TaxID=7151;
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SEQUENCE
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Q64493;
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Matches
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100.0%; 100.0%;

Query Match Best Local Similarity

RESULT 17

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Gaps

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Indels

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Mismatches

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4; Conservative

Matches

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lel SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Chan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Theologis A., Ecker J., Coriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003113; AAF70835.1; -.
PIR; A96650; A96650.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                       Eukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta, Bukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence for Arabidopsis thaliana BAC F2401 from chromosome
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                               Q9MAV4;
01-OCT-2000 (TYENBLrel. 15, Created)
01-OCT-2000 (TYENBLrel. 15, Last sequence update)
01-OCT-2003 (TYENBLrel. 25, Last annotation update)
F2401.6.
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Last sequence update)
Last annotation update)
                                  70 AA
                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress)
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                                  PRELIMINARY;
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Submitted (NOV-1997)
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Submitted (DEC-1997)
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Submitted (JAN-1998)
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Q8TJT0
ID Q8TJT0,
AC Q8TJT0,
DT 01-JUN-2
DT 01-JUN-2
DT 01-JUN-2
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                                  Q9MAV4
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RESULT 21
Q9MAV4
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzaea, Oryza.
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                                                                                                                                                                                                                                            Chironomus pallidivittatus (Midge).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Chironomidea;
Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Lendahl U., Saiga H., Hoeoeg C., Edstroem J.E., Wieslander L.
"Rabid and Concerted Evolution of Repeat Units in a Balbiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAC
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STRAIN-CV. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7,
"Oryza sativa nipponbare(GA3) genomic Archive Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004305; BAC20722.1; -.
SEQUENCE 69 AA; 7836 MW; A7293809EB54E04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 5; Length 69
100.0%; Pred. No. 5.4e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Genetics 117:43-49(1987).
EMEL; X06433; CAA29739.1; -.
NON_TER 69 69
SEQUENCE 69 AA; 7218 MW; 16FA25C6A5644D48 CRC64;
                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
Gamma protein constant region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                   69 AA
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01-MAR-2003 (TrEMBLrel. 23, Cr
01-MAR-2003 (TrEMBLrel. 23, La
01-MAR-2003 (TrEMBLrel. 23, La
P0492E07.18 protein.
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                                                                                                                                  PRELIMINARY;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                                           14 GPRP 17
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            1 GPRP 4
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Q8H408
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                       Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998). BmB1, Z68106; CAA92131.1; -. PINE, T22081; T22081. WormPep; F41E7.8; CE19867. SEQUENCE 72 AA, 7800 MW; 984037B62C980C1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 5; Length 72
100.0%; Pred. No. 5.7e+02;
. Mismatches 0; Indels
                                                                                                                                                                                                                                              Lennard N.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1 73 AA; 7922 MW; 240540A12AA2B117 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
Mixed-lineage Kinase 3 (Fragment).
Rattus norvegicus (Rat).
                                                     Last sequence update)
Last annotation update)
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72 AA.
                                     Created)
PRT;
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                                 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
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 PRELIMINARY;
                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                              F41E7.8 protein.
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                                                                                                                            MEDINE-21929760; PubMed-1193238;

MEDINE-21929760; PubMed-1193238;

MEDINE-21929760; PubMed-1193238;

Galagan J.E., Nuebaum C., Roy A., Emirnov S., Atnoor D., Brown A.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Leigh J.A., Li W., Liu J., Carn I., Graham D.B., Grahame D.A., Guss A.M.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Revev J.N., Smith K.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Revev J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C.,

Rerry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.,

The genome of Methanosarcina acetivorans reveals extensive metabolic

and physiological diversity.,

EMBL; AB011079; AAM07052.1; -.
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"The Bordetella bhu Locus Is Required for Heme Iron Utilization.";
J. Bacteriol. 183:4278-4267 (2001).
A May A VO 32627, A AK 38152.1;
InterPro; IPRO6860; FecR.
Pfam; PF04773; FecR; 1.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligemeceae; Bordetella.
NCBI_TaxID=520;
                       Methanosarcina acetivorans.
Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative cytoplasmic membrane regulatory protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 17; Length 70; 100.0%; Pred. No. 5.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AA.
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STRAIN-UT25;
MEDLINE-21311754; PubMed=11418569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 70 AA;
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Q93M44;
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Matches

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RESULT 23 293M44

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Gaps

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STRAIN-Sprague-Dawley;
Kholodilov N.G., Rzhetskaya M., Burke R.E.;
"Creation of CDNA probes for the Rat MLKs.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY240868; AA091627.1;
GO; GO:0016301; F:kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q86984
Q86984;
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RESULT 24 Q9XVW3

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TISSUB-Liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Cuyang S., Luo L., Bi J.,
Liu M., He F.,
Functional prediction of the coding sequences of 121 new genes
deduced by analysis of cDNA clones from human fetal liver.";
submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF10618; AF71138.1;
SEQUENCE 76 AA, 8424 MW; FBA4E9EB5F2B2EC4 CRC64;
                                                             SEQUENCE FROM N.A.

GENESCA, Loarce Y., Nicolas J.;

de Bustos A., Loarce Y., Nicolas J.;

submitted (NAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ400135; CAB77451.1; -.

NON TER 1 1

NON TER 74 74

SEQUENCE 74 AA; 8020 MW; 0440BC46103E929B CRC64;
                                                                                                                                                                                                                                                                                      Gaps
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Samuel S.J., Jung C.Y.; Continuel S.J., Jung C.Y.; Continued of the promoter-proximal sequence of the 3-hydroxyacyl-Continued of the promoter-proximal sequence of the 3-hydroxyacyl-Continued Gene."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amono sapiena (Human).
Eukaryota, Metazona, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                    Indels
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
3-hydroxyacyl-CoA dehydrogenase isoform 2 (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PICO PRELIMINARY; PRT; 76 AA. Q9PICO; 01-00T-2000 (TrEMBLrel. 15, Created) 01-00T-2000 (TrEMBLrel. 15, Last sequence update) 01-00T-2000 (TrEMBLrel. 15, Last annotation update) PRO2900.
                                                                                                                                                                                                                                                100.0%; Score 25; DB 10;
100.0%; Pred. No. 5.8e+02;
ative 0; Mismatches 0;
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Best Local Similarity 100...
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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60 GPRP 63
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Q9P1C0
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MEDLINE=96187810; PubMed=8614994;
Bausar C.A., Elick T.A., Fraser M.J.;
associated with baculovirus FP mutants derived upon passage in the '368 cell line.";
Virology 21:6:235-237(1996).
Now TER
SEQUENCE 73 AA; 7979 MW; AFBDD75EA52E3ED1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Melamed S., Tanne E., Ben-Haim R., Edelbaum O., Yogev D., Sela I.;
"A Novel Approach to the Study of the Phytoplasma Genome and the Characterization of Sixty Phytoplasmal Genes."
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
Bubmitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
NOW TER.
SEQÜENCE 74 AA, 8678 MW, DBB31EBC94F5B161 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHI.
Hordeum bulbosum (Bulbous barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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100.0%; Pred. No. 5.8e+02;
ative 0; Mismatches 0; Indels
                                                                             ORF2.
Galleria mellonella nuclear polyhedrosis virus (GmNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 28

Q9M3Q3
AC Q9M3Q3
D 01-0CT-2000 (TrEMBLrel. 15, Created)
DT 01-0CT-2003 (TrEMBLrel. 15, Last sequence update)
DT 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
DF 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
DF Chitinase (Fragment).
CM CHI.
CS Hordeum bulbosum (Bulbous barley).
CS Hordeum viridiplantae; Streptophyta; Embryophyta; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0847P0;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Yjcl protein (Fragment).
Aster yellows phytoplasma.
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
Acholeplasmataceae; Phytoplasma.
            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 AA.
          01-NOV-1996 (TrEMBLrel, 01, 01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, Oxf2 (Fragment).
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                SEQUENCE FROM N.A.
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Q847P0
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Length 76;

Score 25; DB 5; Pred. No. 6e+02;

100.0%;

0; Mismatches

4; Conservative

Query Match Best Local Similarity Matches 4; Conserv RESULT 33 à d 8 RX STRATH=Secretally;
RX Adams M.D., Celniker S.E., Holt R.A., Bvans C.A., Gocayne J.D.,
RAdams M.D., Celniker S.E., Holt R.A., Bvans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandall M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,
RA Ballew R.M., Basud M., Baxendale J., Rayaktaroglu L., Beasley E.M.,
Raberon K.W., Benos P.V., Berman B.P., Bandari D., Bollmakov S.,
Borkova D., Borcham M.R., Buluck J., Borckstein P., Borthakov S.,
Borkova D., Borcham M.R., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Bordon K., Doup L.E., Downes M., Dugant Rocha S., Dunkov B.C., Dunn P.,
RA Bortin C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Alockin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hartis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hartis N.L., Harvey D., Helman T.J., Hernandez J.R., Lina Y., Lina X.,
Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.D., Ketchum K.A.,
Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.D., Marken B.,
RA Mount S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelsen M.G.,
Raber R.L. Lei Y., Leviteky A.A., Li J., Mary D.M., Nelsen B.,
Raber B.C., Siden-Kiamos I., Simpson M., Strong R., Sund X.,
Raber B.C., Siden-Kiamos I., Simpson M., Strong R., Sund X.,
Raber B.C., Siden-Kiamos I., Simpson M., Strong R., Sund X.,
Raber B.C., Siden-Kiamos I., Simpson M., Strong R., Sund S., Shir H.,
Raber B.C., Siden-Kiamos I., Simpson M., Strong R., Shir H.,
Raber B.C., Siden-Kiamos I., Simpson M., Strong R., Shir H.,
Raber B.C., Siden-Kiamos I., Simpson M., Strong R., Shir M.,
Raber B.C., Siden-Kiamos I., Shir Roger B.,
Raber B.C., Siden-Kiamos I., Shir Ro ö Gaps . 0 Drosophila melanogaster (Fruit fly). Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Length 76; 0; Indels EMBL; AF001904; AAB58153.1; -. NON TER 76 76 SEQÜENCE 76 AA; 7975 MW; C4E542EB19EDEFEE CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CG14865 protein. Query Match
100.0%; Score 25; DB 4;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0 76 AA. Ephydroidea, Drosophilidae, Drosophila. NCBI_TaxID=7227; PRT; Science 287:2185-2195(2000).
EMBL, AE003708, AAF55162.1; -.
Flybase, FBGT0038314; CG14865.
SEQUENCE 76 AA, 8950 MW, 4 PRELIMINARY; SEQUENCE FROM N.A. 29 GPRP 32 1 GPRP 4 CG14865 Q9VF98 RESULT 31 Q9VF98 S T S

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Lefranc D., Dubucquoi S., Almeras L., De Seze J., Tourvieille B.,
Dussart P., Aubert J.P., Vermersch P., Prin L.;
"Molecular analysis of endogenous retrovirus HRS-1: identification of
frameshift mutations in region encoding putative 28-KDA autoantigen.";
Biochem. Biophys. Res. Commun. 283:437-444(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MAPF303099;
MEDIINE=21082930; PubMed=11214968;
Raneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Natanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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Pred. No. 6.1e+02,
Mismatches 0, Indels
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Carbohydrate kinase.
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2003 (TrEMBLrel. 25,
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SEQUENCE 77 AA; 8223 MW;
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Best Local Similarity luv...
A; Conservative
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1 GPRP 4
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                                                                                                                   RESULT 32
Q9NRK3
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Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBoy R.T., Madpu K., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radume D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Hazen A., Cline R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
Thomsson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
Praser C.M.,
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                       "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
Nature 423.81-86(2003).
BMBL; AB4207; -.
TIGE: AA4207; -.
Hypothetical protein; Complete proteome.
SEQUENCE 78 AA; 8536 MW; F4B455C107BF1C38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Lendahl U., Saiga H., Hoeoeg C., Edstroem J.E., Wieslander L.;
"Rabid and Concerted Evolution of Repeat Units in a Balbiani Ring
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Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
Chironomidae; Chironominae; Chironomus.
NCBI_TaxID=7151;
                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 100.0%; Score 25; DB 16; Length 78; Similarity 100.0%; Pred. No. 6.1e+02; 4; Conservative 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Gamma protein constant region (Fragment).
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EMBL; X06434; CAA29740.1; -.
PIK; S01718; S01718.
NON TER 79 79
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7 GPRP 10
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01-JUN-2003 (
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Q23726
ID Q23726
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081534
1D 08153.
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DT 01-NO
DT 01-NO
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DNA Marcobium japonicum USDA110.";
DNA MP019197-0202).
EMBL, AP005935; BAC42298.1; -
GO, GO:0016810; F:hydrolase activity, acting on carbon-nitrog. . .; IEA.
GO, GO:0016975; P:carbohydrate metabolism; IEA.
InterPro; IPR00250; Polyacc_deacet.
InterPro; IPR01221; Polysacc_deacet.
Complete protecome.
SEQUENCE 77 AA; 8587 MW; C970A6C191E96509 CRC64;
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Kaneko T., Nakamura Y., Sato, S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriquchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Teurucka H., Wada T., Yamada M.,
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MEDLINE=22608414; PubMed=12721629;
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
1011 TaxID=375;
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                                                                                                                                                                         100.0%; Score 25; DB 16; Length 77; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indels
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Bacillus anthracis (strain Ames).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=198094;
  GO, GO:0016301, F:kinase activity, IEA.
InterPro, IPR002173, PfkB.
Pfam, PF00224, pfkB, 1.
PR03TE, PS00584, PFKB, KINASES_2; 1.
KINASE, COMPLEE PROTECTOR SEQUENCE 77 AA, 8223 MW, B9BFSA49ABBC8983 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
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01-070N-2003 (TrEMBLrel. 24, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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Best Local Similarity 100.v
--- 4; Conservative
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SEQUENCE FROM N.A.
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081MP0
AC Q81MP0,
DT 01-UUN-2)
DT 01-UUN-2)
DE HYDCHPET
DE HYDCHPET
DE BAZ207.
OS BAZ207.
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Q89YC1;
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Matches
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
Heller F., Froesner G.G.;
Heller F., Froesner G.G.;
Heller F., Froesner G.G.;
Heller F., Froesner G.G.;
Submitted (BCC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF464084; AAL78626.1; -.
InterPro; IPRO04118; TT_ORF2.
InterPro; IPRO04118; TT_ORF2.
NOW TER
82 82
SEQÜENCE 82 AA; 8946 MW; 4BD430BED7862F56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=genotype III;
MEDLINE=94022306; PubMed=8415646;
Casey J.L., Brown T.L., Colan B.J., Wignall F.S., Gerin J.L.;
"A genotype of hepatitis D virus that occurs in northern South
America.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 12; Length 83; 100.0%; Pred. No. 6.5e+02; cive 0; Mismatches 0; Indels
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                       08QY94 PRELIMINARY; PRT; 82 AA. 08QY94; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) 0RF2 (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heparitis delta antigen (Fragment).
                                                                                                                                                                                          TT virus.
Viruses; ssDNA viruses; Circoviridae; Anellovirus.
NCBI_TaxID=68887;
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EMBL; L22064; AAB02602.1; -.
GO; GO:0042025; C.host cell nucleus; IEA.
GO; GO:0003723; F.RNA binding; IEA.
InterPro; IPR002506; HDV_ag.
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ProDom; PD002887; HDV ag; 1.
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Viruses; Deltavirus.
NCBI_TaxID=12475;
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Best Local Similarity 100.0
Local 4; Conservative
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Best Local Similarity 10v.v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 GPRP 59
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Q81845;
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Q81839;
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ID Q8
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glucose transporter type four (Fragment).
Bubalus bubalis (Domestic water buffalo).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Eutheria, Ceratiodactyla, Ruminantia, Pecora; Bovoidea; Bovinae; Bubalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Patil S.S.B., Totey S.S.M.;
"Partial cDNA sequence of glucose transporter type four of Bubalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 10; Length 80; 100.0%; Pred. No. 6.3e+02; tive 0; Mismatches 0; Indels
Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
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100.0%; Score 25; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                      SEQUENCE FROM N.A.

Veronesi C., Thalouarn P.;

"Sugarcane resistance to Striga hermonthica.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF079174; AAC27797.1;

HSSP; P30074; 1D6F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 AA; 8744 MW; 7B94776D2A46F418 CRC64;
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                                                                                                                                                                                                                                                                      GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
InterPro; PRR01099; N.C. synthase.
Pfan; PF00195; Chal stil synt; 1.
ProDom; PD000453; N-C. synthase; 1.
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Best Local Similarity
Matches 4; Conserv
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                                                       NCBI_TaxID=4547;
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SEQUENCE
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Sugimoto K., Hirochika H., Minobe Y., Kawamata H., Hibi T., Nanba Yamashita S., Tsuchizaki T.,
Yamashita S., Tsuchizaki T.,
"Nucleotide sequence of cloned Miscanthus streak virus DNA.";
Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; D00800; BAA25577.1; --
SEQUENCE 84 AA; 8721 MW; BS7A04C249776BIC CRC64;
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STRAIN=MAFF30309;
MEDLINE=2030; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto
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                                                                                                                               SEQUENCE FROM N.A.
Chatani M., Matsumoto Y., Mizuta H., Ikegami M., Boulton M.I.,
Davies J.W.;
                                                                                                                                                                                         "The nucleotide sequence and genome structure of Geminivirus
                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 12; Length 84; 100.0%; Pred. No. 6.6e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 12; Length 84; 100.0%; Pred. No. 6.6e+02; ative 0; Mismatches 0; Indels
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                       Miscanthus streak virus.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBU databases.
EMBL, 701030; BAA00837.1; -.
PIR, 201356; J01356.
SEQUENCE 84 AA; 8751 MW; ABCCDFB249776BIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY; PRT; 86 AA.
Q98AH9;
Q1-OCT-2001 (TrEMBLrel. 18, Created)
Q1-OCT-2001 (TrEMBLrel. 18, Last sequence update)
Transposase.
MSRS992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                072913;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0RF VI.
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
0RF VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miscanthus streak virus.
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=10825;
                                                                         Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBI_TaxID=10825;
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Best Local Similarity 100.0
Matches 4, Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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                                                         Miscanthus streak virus.
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072913
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01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-MAR.2003 (TrEMBLrel. 23, Last annotation update)
01-MAR.2003 (TrEMBLrel. 23, Last annotation update)
Membrane cofactor protein (Fragment).
Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Clordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Testis;
MEDLINE=22309086; PubMed=12421914;
Riley R.C., Tannenbaum P.L., Abbott D.H., Atkinson J.P.;
Riley R.C., Tannenbaum P.L., Abbott D.H., Atkinson J.P.;
"Cutting Edge: Inhibiting Measles Virus Infection but Promoting Reproduction: An Explanation for Splicing and Tissue-Specific Expression of CD46.";
J. Immunol. 169:5405-5409(2002).
BMBL; AN157982; AAN64664.1; -.
SEMEL: AN157982; AAN64664.1; -.
SEQÜENCE 84 AA; 9279 WW; CCSEA7ACS9AED187 CRC64;
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STRAIN=genotype III;
MEDLINE=94022306; PubMed=8415646;
Casey J.L., Brown T.L., Colan E.J., Wignall F.S., Gerin J.L.;
"A genotype of hepatitis D virus that occurs in northern South America.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 25; DB 12; Length 83; Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-DEC-2001 (TrEMBLrel.19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatitis delta antigen (Fragment).
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Q67593
1D Q67593 PRELIMINARY; PRT;
AC Q67593;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                           Hepatitis delta virus (HDV).
Viruses; Deltavirus.
VicBL_TaxID=12475;
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Q8HYY0
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Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
                                                                                                                                             Query Match 100.0%; Score 25; DB 16; Length 86; Best Local Similarity 100.0%; Pred: No. 6.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                          86 AA; 9502 MW; 7A9FBCF466863A1C CRC64;
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Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10298;
                                                                                                                                                                                                                                                                                                                                                                        Q845Q9 PRELIMINARY; PRT; 87 AA. Q845Q9; O1-JUN-2003 (TrEMBLrel. 24, Created) O1-JUN-2003 (TrEMBLrel. 24, Last sequence update) O1-OCT-2003 (TrEMBLrel. 25, Last annotation update) Relaxase /helicase (Fragment).
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Last annotation update)
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100.0%; Score 25; DB 2; Lu
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0;
      GO; GO:0006118; P:electron transport; IEA
                          InterPro; IPR003816; Nitrate_red_gam.
Pfam; PF02665; Nitrate_red_gam; I.
Hypothetical protein; Complete proteome.
NON TER 86
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01-MAY-1997 (TrEMBLrel. 03, Last seqn
01-DEC-2001 (TrEMBLrel. 19, Last ann
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Human herpesvirus 1.
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SEQUENCE
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Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorbizobium loti.",
DNA Res. 7:331-338(2000).
EMBL; AP003008; BAB52351.1; -.
InterPro; IPR001207; Trnspsase mutatr.
Pfam; PF00072; Transpo_mutator; 1.
Complete proteome.
SEQUENCE 86 AA; 9753 MW; 3AIDFC5DAD1763D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinsshi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                  Gaps
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 16; Length 86; 100.0%; Pred. No. 6.7e+02; Live 0; Mismatches 0; Indels
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Nature 417:141-147(2002).
EMBL; AL939105; CAB58278.2; -
GO; Go:0009325; C:nitrate reductase complex; IEA.
GO; GO:0008940; F:nitrate reductase activity; IEA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequen
01-JUN-2003 (TrEMBLrel. 24, Last annota
Hypothetical protein SC00518 (Fragment)
SC00518 OR SCF6.14.
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MEDLINE=97000351; PubMed=8843436;
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STRAIN=A3(2) / M145;
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STRAIN=2402-89.
Shorum H., L'Abbee-Lund T.W., Solberg A., Wold A.;
Sorum H., L'Abbee-Lund T.W., Solberg A., Wold A.;
The integron containing IncU R plasmids pRAS1 and pAr-32 from the fish pathogen Aeromonas salmonicida.",
Antimicrob Agents Chemother. 47:1285-1290(2003).
BMBL; AB37790; Cab57190.1, -
BMBL; AB37790; Cab57190.1, -
GQO; GO:0046821; C:extrachromosomal DNA; IEA.
GQO; GO:004386; F:helicase activity; IEA.
NON TER.
SEQÜENCE 87 AA, 9759 MW; SOBA3ACS8103DIAZ CRC64;
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STRAIN-Jura;
STRAIN-Jura;
MEDLINE-92219360; PubMed-1313901;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
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MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
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MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
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MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces V., Schwyzer M.;
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MITCH U.V., Fraefel C., Vogt B., Vlcek C., Paces 
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MEDLINE=21128732; PubMed=11234002;
COLB S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
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Mycobacterium leprae.
Bacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769;
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Schwyzer M., Paces V., Letchworth G.J., Misra V., Buhk H.J.,
Lowery D.E., Simard C., Bello L.J., Thiry B., Vicek C.;
"Complete DNA sequence of bovine herpesvirus 1.";
Submitted (SRP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ004801; CAA06136.1; -
SEQUENCE 87 AA; 9550 MW; 9703325A10D22897 CRC64;
                                                                                                                                                                                                        'Match 100.0%; Score 25; DB 12; Length 87; Local Similarity 100.0%; Pred. No. 6.8e+02; les 4; Conservative 0; Mismatches 0; Indels
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Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1996).
EMBL; U70039; AAB37296.1; -.
SEQUENCE 87 AA; 9466 MW; DDB3024B6D178483 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine herpesvirus type 1 (strain Jura).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
VCBI_TaxID=31518;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ML2035.
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AC 09CBF6;
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DT 01-UN-2
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DE HYPCCHET
GN MYCOBGC,
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CC COTTOBG
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Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Felrewell T., Farser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Murter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Moodward J.R.,
Massive gene decay in the leprosy bacillus.";
In Marsive gene decay in the leprosy bacillus.";
Massive gene decay in the leprosy bacillus.";
In Mature 409:1007-1011(2001).
BMBL, ALS83924; CAC30990.1;
BMSL, RSMIG3; F87163.
BTR, F87163; F87163.
BTR, F87163; F87163.
BY PROTECTION PROCESTANCE BY AB. 9917 MW; 90697B6FD9BADBEB CRC64;
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              6019581 segs, 976053577 residues
                                                                                                                       using sw model
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Maximum Match 100%
Listing first 65 summaries
                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                          US-09-931-009A-2
25
1 GPRP 4
                                                                                                                       - protein search,
                                                                                                                                                                   September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 4
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and is derived by
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                                                                                                                                                                                                                                                          Title:
Perfect score:
Sequence:
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Sequence 1153, Ap Sequence 1153, Ap Sequence 1, Appli Sequence 13, Appli Sequence 35, Appl Sequence 35, Appl Sequence 36, Appl Sequence 36, Appli Sequence 36, Appli Sequence 28, Appli

Sequence 3, Appli Sequence 5, Appli Sequence 2, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 25, Appli Sequence 25, Appli Sequence 21, Appli Sequence 101, Appli Sequence 111, Appli Sequence 112, Appli Sequence 115, Appli Sequence 331, Appli Sequence 115, Appli Sequence 331, Appli Sequence 115, Appli

RESULT 1 PCT-US03-07665-1 ; Sequence 1, Application PC/TUS0307665

Description

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Query Match Length DB

Score

Result ٥ ا

SUMMARIES

ALIGNMENTS

Appl Appl Appl

Sequence Sequence Sequence

Sequence Seq

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1 GPRP 4
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; Sequence 1, Application PC/TUS0324864
; GENERAL INFORMATION:
    APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
    APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
    APPLICANT: BRESAGEN, LTD.
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL DIFFERENTIATION
    TITLE OF INVENTION: OF EMBRYONIC STEM CELLS
    FILE REFERENTE: 1865-002-08-08
    CURRENT APPLICATION NUMBER: PCT/US03/24864
    CURRENT APPLICATION NUMBER: US 60/401,968
    PRIOR APPLICATION NUMBER: US 60/401,968
    PRIOR APPLICATION NUMBER: US 60/459,090
    PRIOR PILING DATE: 2002-08-08
    NUMBER OF SEQ ID NOS: 5
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GENERAL INFORMATION:
APPLICANT: BRESAGEN, LTD.
APPLICANT: MEDICAL COLLEGE OF GEORGIA RESEARCH INSTITUTE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENRICHMENT OF NEURAL STEM
TITLE OF INVENTION: CELLS USING CERAMIDE ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
APPLICANT: BRESAGEN LIMITED
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRIMATE NEURAL
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: 18465-0023
CURRENT FILING DATE: 2003-03-13
PRIOR APPLICATION NUMBER: PCT/US03/07665
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO II
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4;
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100.0%; Score 25; DB 1; L
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use FILE REFERENCE: UNGR-1536
CURRENT PAPLICATION NUMBER: PCT/US98/27060
CURRENT FILING DATE: 1998-12-17
BARLIER APPLICATION NUMBER: 08/993,165
BARLIER APPLICATION NUMBER: 08/993,165
SARLIER PILING DATE: 1997-12-18
SOFTWARE: PATEIN VOX: 42
SOFTWARE: PATEIN VOX: 42
SOFTWARE: PATEIN VOX: 42
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TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
CURRENT APPLICATION 1998-12-17
NUMBER OF SEQ ID NOS: 40
SEQ ID NOS: 40
SEQ ID NO 6
LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: peptide PCT-US03-30112-1
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100.0%; Score 25; DB 1; L
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 25; DB 1; I
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: PCT/US03/30112
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: 08 60/413,510
PRIOR FILING DATE: 2002-09-25
PRIOR FILING DATE: 2003-07-07
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application PC/TUS9827060A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US98-27060-6; Sequence 6, Application PC/TUS9827060; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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JOS-08-20-514-4

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mult. Thomas W.
APPLICANT: Milt. Thomas W.
APPLICANT: Ginsberg, Mark H.
APPLICANT: Ginsberg, Mark H.
APPLICANT: Cont. Yi-Ping
APPLICANT: O'TOOLe, Timothy E.
TITLE OF INVENTION: Structural Models for Cytoplasmic
TITLE OF INVENTION: Domains of Transmembrane Receptors
NUMBER OF SEQUENCES: 20
TITLE OF INVENTION: Domains of Transmembrane Receptors
NUMBER OF SEQUENCES: 20
SCHESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
STREET: 1150 Santa Monica Boulevard, Suite 400
STREET: LOS Angeles
STATE: California
COUNTRY: USA
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS #1.0, Version #1.25
SUFURBIT APPLICATION DATA:
TURNENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/260,514
FILING DATE: USONDANTON.
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                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
SOFTWARE: Word 5.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,820
FILING DATE: 15-COT-1993
CLASSIFICATION NUMBER: 33,862
ATTORNEY/AGENT INFORMATION:
NAME: Darkes, Paul R.
REFERENCE/DOCKET NUMBER: 33,862
REFERENCE/DOCKET NUMBER: 3158
TELEPHONE: (215) 454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTER.451CS:
LENGTH: 4 amino acids
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NAME: Farber, Michael B.
REGISTRATION NUMBER: 32,612
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                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.

Matches 4; Conservative
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TOPOLOGY:
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; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence PCT-US98-27060-6
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLES OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLES OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILLON, FALLON, LUNGMUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: G606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/705,071
FILLING DATE: 19910234
CLASSIFICATION #125
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GENERAL INFORMATION:
APPLICANT: Klein, Scott I.
APPLICANT: Molino, Bruce F.
TITLE OF INVENTION: ANTITHROMBOTIC AZACYCLOALKYLALKANOYL.
TITLE OF INVENTION: PEPTIDES AND PSEUDOPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
                                                                  100.0%; Score 25; DB 1; Length 4; 100.0%; Pred. No. 5.5e+06; ative 0; Mismatches 0; Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 3; Length 4; 100.0%; Pred. No. 5.5e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/07705071 GENERAL INFORMATION:
                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-705-071-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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APPLICANT: Machine Jr., Francis S.
APPLICANT: Bush, Larry R.
APPLICANT: Swenson, Stephen
APPLICANT: Swenson, Stephen
TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC
TITLE OF INVENTION: ACTIVITY
WUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4;
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Sequence 3, Application US/09040712
GENERAL INFORMATION:
APPLICANT: Dien, Theodore T.
APPLICANT: Lie, Theodore T.
APPLICANT: Ratnikov, Boris I.
APPLICANT: Milman, Robert S.
APPLICANT: Smith, Jeffrey W.
TITLE OF INVENTION: AGGLUTRIMETRIC ASSAYS IN BLOOD FILE REFERENCE: 22608-001491
CURRENT APPLICATION NUMBER: US/09/040,712
CURRENT PLING DATE: 1998-03-18
PRIOR APPLICATION NUMBER: US 08/820,999
PRIOR FILING DATE: 1997-03-20
NUMBER OF SEC'ID NOS: 3
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/982,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 25; DB 13;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERNES/COCKET NUMBER: DITI 124.1
TELECOMMUNICATION INFORMATION:
TELEFAX: 603 437 8977
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/753,781
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      Sequence 1, Application US/08982981 GENERAL INFORMATION:
                                                                                                                                                                                                                                                         ADDRESSEE: Diatide, Inc. STREET: 9 Delta Drive CITY: Londonderry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-08-982-981-1
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TOPOLOGY: li
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                      ÌS-08-982-981-1
                                                                                                                                                                                                                                                                                                                           STATE:
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APPLICANT: Bush, Larry R
APPLICANT: Swenson, Stephen
APPLICANT: Sanchez, Bladio F
TITLE OF INVENTION: Thrombolytic Agents with Antithrombotic
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4;
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100.0%; Score 25; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: FIDEPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/753,781B
PILING DATE: 02-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NOONAN, Kevin E
REGISTRATION NUMBER: 96,2056
TELEPRATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRAK: 312 913 0001
                                                                                                                                                                                             ORGANISM: Ligand sequence recognized by integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 25; DB 11;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08753781B GENERAL INFORMATION:
                                                                      NOLECULE TYPE: peptide HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SURCE: ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 4 amino acids
amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: MCDonn
STREET: 300 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-753-781B-2
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US-09-593-117-6

Sequence 6, Application US/09593117

SERNEAL INFORMATION:

APPLICANT: Evan C., Unger

APPLICANT: Way, Yungiu

TITLE OF INVENTION: Optacoustic Contrast Agents ANd Methods For Their Use

TITLE OF INVENTION: Optacoustic Contrast Agents AND Methods For Their Use

TITLE OF INVENTION: Optacoustic Contrast Agents AND Methods For Their Use

FILE REFERENCE: UNGRI594

CURRENT FILING DATE: 2002-06-18

PRIOR FILING DATE: 2002-06-18

PRIOR FILING DATE: 1997-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin version 3.1

INVICTION OF
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                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-218-660-4
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US-09-376-529-2

Sequence 2, Application US/09376529

Sequence 2, Application US/09376529

GENERAL INFORMATION:
TITLE OF INVENTION: Imaging with TC-99 Labeled
TITLE OF INVENTION: Fibrin-Alpha-Chain Peptide
FILE REFERENCE: THAO1.NP003

CURRENT FILING DATE: 1999-08-18

PRIOR APPLICATION NUMBER: 60/096,803

PRIOR PLILING DATE: 1998-08-18

PRIOR PLILING DATE: 1998-08-18

SOFTWARE: FastSEQ for Windows DEMONSTRATION Version 4.0

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4;
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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, OTHER INFORMATION: Synthetic construct US-09-593-117-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
GRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Unknown
US-09-376-529-2
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ORGANISM: Artificial Sequence
                                                                              TYPE: PRT
ORGANISM: Artificial Seguence
       PatentIn Ver. 2.1
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Best Local Similarity
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  SOFTWARE: 1
SEQ ID NO 4
LENGTH: 4
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GENERAL INFORMATION:
APPLICANT: Unger, Evan C
APPLICANT: Shen, Dekang
APPLICANT: Shen, Dekang
APPLICANT: Wu, Guanli
ITILE OF INVENTION: Therapeutic Use
ITILE OF INVENTION: Therapeutic Use
FILE REFERENCE: DUP-0307
CURRENT FILING DATE: 1998-12-22
FRIOR APPLICATION NUMBER: 08/660,032
FRIOR APPLICATION NUMBER: 08/660,032
FRIOR APPLICATION NUMBER: 08/660,032
FRIOR FILING DATE: 1996-06-06
FRIOR FILING DATE: 1996-06-06
FRIOR FILING DATE: 1996-06-01
FRIOR FILING DATE: 1996-06-01
FRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 22
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Sequence 5, Application US/09091578B

GENERAL INFORMATION:

APPLICANT: MADISON:

APPLICANT: SMITH, JEFFREY W.

TITLE OF INVENTION: TARGETED THERAPEUTIC OR DIAGNOSTIC

TITLE OF INVENTION: AGENTE AND METHODS OF MAKING AND USING SAME

FILE REFERENCE: 19191.0002

CURRENT APPLICATION NUMBER: US/09/091,578B

CURRENT PILING DATE: 1998-06-19

PRIOR APPLICATION UNMBER: PCT/US96/20577

PRIOR APPLICATION UNMBER: PCT/US96/20577

PRIOR APPLICATION UNMBER: 60/009,028

PRIOR APPLICATION NUMBER: 1995-12-19

SPIOR FILING DATE: 1995-12-21

NUMBER OF SEQ ID NOS: 5

LENGTH: 4
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
CHER INFORMATION: GPRP Peptide
NAME/KEY: BEPTIDE
LOCATION: (1)..(4)
CHER INFORMATION: Peptide inhibitor of fibrin polymerization.
US-09-040-712-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence; Note; OTHER INFORMATION: artificial construct
US-09-091-578B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 14; Length 4; 100.0%; Pred. No. 5.5e+06; vative 0; Mismatches 0; Indels
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100.0%; Score 25; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
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General A Application US/09699679A

General INFORMATION:
APPLICANT: Unger, Evan C.
APPLICANT: Unger, Evan C.
APPLICANT: Shen, Dekang
APPLICANT: Wu, Guanli
TITLE OF INVENTION: Novel Targeted Compositions For Diagostics And Therapeutic Use
FILE REPRENCE: UNGRISSER: 08/69,679A
CURRENT APPLICATION NUMBER: US/09/699,679A
CURRENT FILING DATE: 1998-12-22
FRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-06-06
PRIOR PELING DATE: 1996-05-01
PRIOR PELING DATE: 1996-05-01
PRIOR PELING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
SPRIOR FILING DATE: PARENTEN NUMBER: OR SEQ ID NOS: 24
LENGTH: 4
LENGTH: 4
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                                                                                                                          FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-687-156A-1
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Sequence 2, Application US/09763777B

GENERAL INPORMATION:
TITLE OF INVENTION: Imaging with TC-99m Labeled Fibrin Alpha
TITLE OF INVENTION: Chain Peptide
FILE REFERENCE 831-119
CURRENT APPLICATION NUMBER: US/09/763,777B

CURRENT FILING DATE: 1999-08-17

PRIOR APPLICATION NUMBER: US 60/096,803

PRIOR APPLICATION NUMBER: US 60/096,803

PRIOR FILING DATE: 1998-08-17

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0
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Similarity 100.0%; Score 25; DB 20;
Similarity 100.0%; Pred. No. 5.5e+06;
4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic construct
                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                            1 GPRP 4
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US-09-699-679A-4
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                           SEQ ID NO 1
LENGTH: 4
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APPLICANT: Sherbine, James P.
APPLICANT: Sherbine, James P.
APPLICANT: Sherbine, James P.
APPLICANT: Sledeski, Adam W.
TITLE OF INVENTION: STABLE NON-HYGROSCOPIC CRYSTALLINE FORM OF N-[N-[N-(4-(PIPERIDIN-TITLE OF INVENTION: YI) BUTPANOYL)-N-ETHYLGLACKTYL]-L-BETPA-CYCHOHEXYL ALANINE ATTLE OF INVENTION: INTERMEDIATES THERRED'S, AND PEPPARATION THEREOF AND OF ANTITHROME TITLE OF INVENTION: AZACYCLOALKYLALKANOYL PEPTIDES AND PSEUDOPEPTIDES
TITLE OF INVENTION: AZACYCLOALKYLALKANOYL PEPTIDES AND PSEUDOPEPTIDES
CURRENT APPLICATION NUMBER: US/09/639, 634A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence;
PEATURE:
OTHER INFORMATION: synthetic peptide capable of inhibiting binding of fibrinogen to;
OTHER INFORMATION: platelets
US-09-639-634A-4
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GENERAL INFORMATION:
APPLICANT: Thaler, David S
APPLICANT: Thaler, David S
APPLICANT: MESSMEr, Bradley T
TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
CURRENT APPLICATION NUMBER: US/09/687,156A
CURRENT FILING DAIE: 2000-10-13
NUMBER OF SEQ ID NOS: 91
  Gaps
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/251,030
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1997-08-21
PRIOR FILING DATE: 1997-08-21
PRIOR APPLICATION NUMBER: 60/024,284
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                Salazar , Diane (Deceased)
Salazar , Richard (Legal )
                                                                                                                                                                                                                                                                                       APPLICANT: Aventis Pharmaceuticals Inc.
APPLICANT: Chrzan, Zofia J
APPLICANT: Mencel, James J
APPLICANT: Toledo-Valasquez, David
APPLICANT: Windisch, Vincent
APPLICANT: Woodward, Rick G.
                                                                                                                                                                                                                                  Sequence 4, Application US/09639634A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vemuri, Narasimha M
Gardetto, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matthew, Powers R.
Kubiak, Gregory G.
Liu, Robert C.
  4; Conservative
                                                     1 GPRP 4
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US-09-687-156A-1
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     Matches
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US-10-016-569A-25
US-10-016-569A-25
US-10-016-569A-25
US-10-016-569A-25
US-10-016-569A-25
SEQUENCE 25. Application US/10016569A
SEDERAL INFORMATION:
APPLICANT: Tendy, Ching-Gung
APPLICANT: Chen, Li-Jung
APPLICANT: Chen, Li-Jung
APPLICANT: Shih, Kea-Shyang
ITILE OF INVENTION: Conjugates Synthesized Thereby and Targeted Lippid Conjugates,
ITILE OF INVENTION: the Same
FILLE REPERRANCE: P13/9
CURRENT APPLICATION NUMBER: US/10/016,569A
CURRENT PILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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US-10-046-801-6
SEQUENCE 6, Application US/10046801
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TITLE REPERENCE: UNGRISS2
FILE REPERENCE: UNGRISS2
CURRENT APPLICATION NUMBER: US/10/046,801
                                                                                               RESULT 22
US-09-931-009A-2
Sequence 2, Application US/09931009A
GENERAL INFORMATION:
TITLE OF INVENTION:
PRO-INFLAMMATORY FIBRINOPEPTIDE
FILE REFERENCE:
CURRENT APPLICATION WIMBER: US/09/931,009A
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 2
LENGTH: 4
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100.0%; Pred. No. 5.5e+06;
attive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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CORGANISM: Human Cell
US-10-016-569A-25
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1 GPRP 4
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US-09-813-484-6
Sequence 6, Application US/09813484
Sequence 6, Application US/09813484
Sequence 6, Application US/09813484
Sequence 6, Application US/09813484
SEQUENCE FOR INVERTION:
TITLE OF INVERTION: Filled Compositions
TITLE OF INVERTION: Filled Compositions
TITLE OF INVERTION: Filled Compositions
FILE REFERENCE: UNGRIGOD
CURRENT APPLICATION NUMBER: US/09/813,484
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/929,847
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09779054
GENERAL INFORMATION:
APPLICANT: Lu, Xinjie
CURRENT ELE REFERENCE: A-70312/TAL/ANS
CURRENT APPLICATION NUMBER: US/09/779,054
CURRENT APPLICATION NUMBER: GB 0002625.2
PRIOR PILING DATE: 2000-02-05
PRIOR FILING DATE: 2000-02-05
RIOR PRIOR FILING DATE: 2000-02-05
ROWHERE PATENTIN VERSION 3.0
SEQ ID NO 16
LENGTH: 4
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                                             FEATURE: PEATURE: ) OTHER INFORMATION: Analog of N-terminus tripeptide identified in SEQ ; CTHER INFORMATION: ID NO: 1 US-09-763-777B-2
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100.0%; Score 25; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Completely synthetic sequence US-09-813-484-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: thrombin-binding sequence US-09-779-054-16
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ORGANISM: Artificial Seguence
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 4; Conservative
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US-09-779-054-16
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                                      ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide US-10-674-756-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 27
PCT-1502-29660-101
Sequence 101, Application PC/TUS0229060.
GENERAL INFORMATION:
APPLICANT: The Burnham Institute
APPLICANT: Smith, Jeffrey W.
APPLICANT: Smith, Jeffrey W.
TILLE OF INVENTION: Selective Substrates for Matrix TITLE OF INVENTION: Selective Substrates for Matrix CHERE OF INVENTION: Metalloproteinases
FILE REFERENCE: FP-LJ 5413
CURRENT APPLICATION NUMBER: PCT/US02/29060
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 09/953,592
PRIOR APPLICATION NUMBER: US 09/953,592
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
LEMPTH. 1.
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APPLICANT: Chen, Emily I.
APPLICANT: Kridel, Steven J.
TITLE OF INVENTION: Selective Substrates for Matrix
FITLE OF INVENTION: Metalloproteinases
FILE REFERENCE: P-LJ 4851
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100.0%; Score 25; DB 31;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: synthetic construct PCT-USO2-29060-101
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; Sequence 101, Application US/09953592
; GENERAL INFORMATION:
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APPLICANT: Teng, Chin-Lu
APPLICANT: Teng, Chin-Lu
APPLICANT: Chang, Ting-Gung
APPLICANT: Chang, Ting-Gung
APPLICANT: Chen, Li-Jung
APPLICANT: Chen, Li-Jung
APPLICANT: Shih, Kea-Shyang
APPLICANT: Conjugates Synthesized Thereby and Targeted Liposomes Containing
FILE REFERENCE: 103/10/308,644
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 4
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100.0%; Score 25; DB 26;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 29;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US/09/540,448
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 08/925,353
PRIOR RILING DATE: 1997-09-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
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US-09-868-677-13

Sequence 13, Application US/09868677

GENERAL INFORMATION:
APPLICANT: Samuel Davis, Nicholas W. Gale, George D. Yancopoulos, and
APPLICANT: Neil Stahl
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL ACTIVITY OF LIGANDS
FILE REFERENCE: REG 670-A-US
CURRENT APPLICATION NUMBER: US/09/868,677
CURRENT PILING DATE: 2002-02-08
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-12-23
Sequence 2, Application US/07884495
GENERAL INFORMATION:
APPLICANT: Tan, Paris Som Tjwan
APPLICANT: Tan, Paris Som Tjwan
APPLICANT: Tan, Paris Som Tjwan
APPLICANT: Maings, Wilhelmus Nicolaas
ITILE OF INVENTION: PROTEIN FROM LACTIC ACID BACTERIA
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
COUNTRY: New York
COUNTRY: United States of America
ITILIANTED: DOILS
ITILIANTED:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,495
FILING DATE: 19220515
CLASSIPICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 1931
ATTORNEY/AGENT INFORMATION:
NAME: MOTAN: THOMBER: E-MAX-1991
REFERENCE/DOCKET NUMBER: 2805/41484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PCT-USO2-2-115
SQUENCE 115, Application PC/TUSO224572
SQUENCE 115, Application PC/TUSO224572
GGENERAL INFORMATION:
APPLICANT: Bright, Gary R.
APPLICANT: Bremkumar, D. David
TITLE OF INVENTION: Positional Biosensors for the Assay of Cellular Biochemistry;
FILE REFERENCE: 01-1020-PCT
CURRENT PLING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR APPLICATION NUMBER: 60/341,589
PRIOR PLING DATE: 2001-08-01
PRIOR PLING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 115
LENGH: 4
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Emily I.
APPLICANT: Chen, Emily I.
APPLICANT: Chen, Emily I.
TITLE OF INVENTION: Selective Substrates for Matrix TITLE OF INVENTION: Metalloproteinases
FILE REFERENCE: P-LJ 5432
CURRENT APPLICATION NUMBER: US/10/243,613
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: US 09/953,592
PRIOR PLING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PSECE OF Windows Version 4.0
SEQ ID NO 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-10-243-613-101
                                                                                                                                                                                                                                             5-10-243-613-101
Sequence 101, Application US/10243613
GENERAL INFORMATION:
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RESULT 31

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APPLICANT: Conley, Michael
APPLICANT: Bulter, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Screen for Agents
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Screen for Agents
TITLE OF INVENTION: Modify Feeding Behavior
TITLE OF INVENTION: ONDER: 002-09-24
CURRENT APPLICATION NUMBER: 007324,406
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 352
SOFTWARE: Patentin version 3.1
FROM IN 0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cowley, Michael
APPLICANT: Come, Roger
APPLICANT: Come, Roger
APPLICANT: Low, Malcolm
APPLICANT: Low, Malcolm
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Be?
FILE REFERENCE: 899-63986
CURRENT APPLICATION NUMBER: PCT/US02/30533A
CURRENT FILING DATE: 2002-09-24
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Polypeptide variation PCT-US02-30533-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 331, Application PC/TUS0230533A GENERAL INFORMATION:
                                                                                                                                                                                     Sequence 331, Application PC/TUS0230533 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION: Molecules that Modulate Ubiquitin-Dependent Proteclysis and
TITLE OF INVENTION: Methods for Identifying Same
FITLE OF INVENTION: Methods for Identifying Same
FILE REFERENCE: MTS1-P01-011
CURRENT APPLICATION NUMBER: US/10/275,427A
CURRENT APPLICATION NUMBER: US/10/276,427A
PRIOR APPLICATION NUMBER: OTT/CA01/00632
PRIOR APPLICATION NUMBER: PCT/CA01/00632
PRIOR FILING DATE: 2001-05-04
SOFTWARE: Patentin version 3.1
SEQ ID NO 34
LENGTH: 4
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US-10-211-088-115
Sequence 115 Application US/10211088
Sequence 115 Application US/10211088
Sequence 115 Application US/10211088
SEQUENCE 115 Application US/10211088
TERENT ENGRATION: Over I Fusion Proteins And Assays For Molecular Binding FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT APPLICATION NUMBER: US/10/211,088
FRIOR FILING DATE: 2002-10-15
PRIOR PILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin Version 3.1
SEQ ID NO 115
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     DB 23; Length 4; 5.5e+06;
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0;
Query Match 76.0%; Score 19; DB Best Local Similarity 75.0%; Pred. No. 5.5¢ Matches 3; Conservative 0; Mismatches
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(S-10-275-427A-34)
(Sequence 34, Application US/10275427A)
(GENERAL INFORMATION:
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                                                                                                                                                               1 GPAP 4
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Gaps

1 GPR 3

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## APPLICANT: Conjuchem, Inc.
## APPLICANT: Bridon, Dominique
## APPLICANT: Bridon, Dominique
## APPLICANT: Bridon, Dominique
## APPLICANT: Bridon, Alan
## APPLICANT: Milner, Peter
## APPLICANT: Thibandeau, Karen
## APPLICANT: 2110
## APPLICANT: 100 COMPONENTS
## TITLE OF INVENTION: COMPONENTS
## TITLE OF INVENTION: COMPONENT: 0/134,406
## PRIOR PLILNG DATE: 1999-09-10
## PRIOR PLILNG DATE: 1999-09-10
## PRIOR PLILNG DATE: 1999-09-10
## PRIOR FILING DATE: 1999-10-18
## NUMBER OF SEQ ID NOS: 1617
## SEQ ID NOS: 1617
## SEQ ID NO 1153
## APPLICANTON WORLD
#
                                                                                          APPLICANT: Ocniuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
APPLICANT: Thibaudeau, Karen
APPLICANT: Thibaudeau, Karen
APPLICANT: Thibaudeau, Karen
APPLICANT: ComPONENTS
TITLE OF INVENTION: COMPONENTS
TITLE OF INVENTION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SEQ ID NO 1153
ILENGTH: 3
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic
CTHER INFORMATION: Peptide
US-09-623-548A-1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.0%; Score 18; DB 20; Length 3; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 3; Conservative 0; Mismatches 0; Indels
                      ; Sequence 1153, Application US/09623548A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-657-276-1153
; Sequence 1153, Application US/09657276
; GENERAL INFORMATION:
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US-09-376-529-1
Sequence 1, Application US/09376529
GENERAL INFORMATION:
APPLICANT: Thakur, Madhukar L.
TITLE OF INVENTION: Imaging With TC-99 Labeled
TITLE OF INVENTION: Fibrin-Alpha-Chain Peptide
FILE REFERENCE: THAQ1. ND03
CURRENT APPLICATION NUMBER: US/09/376,529
CURRENT FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 60/096,803
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows DEMONSTRATION Version 4.0
SEQ ID NO 1
LENGTH: 3
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72.0%; Score 18; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels
Sequence 331, Application PC/TUS0231944A

Sequence 331, Application PC/TUS0231944A

GENERAL INFORMATION:
APPLICANT: Imperial College Innovations Limited
APPLICANT: Bloom, Stephen R.
APPLICANT: Ghatei, Mohammad A.
APPLICANT: Ghatei, Mohammad A.
APPLICANT: Ghatei, Mohammad A.
APPLICANT: Coney, Michael
APPLICANT: Coney, Michael
APPLICANT: Coney, Michael
APPLICANT: Coney, Malcolin
APPLICANT: Now Malcolin
APPLICANT: Now Malcolin
APPLICANTON WHORER: DCT/US02/31944A
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR APPLICATION NUMBER: US 60/392,109
PRIOR PILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 335

SSCTWARE: PatentIn version 3:1
LENGTH: 3
LENGTH: 3
LENGTH: 3
LENGTH: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANIGM: Artificial Sequence
PEATURE:
COTHER INFORMATION: Unknown
US-09-376-529-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
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TYPE: PRT ORGANISM: Artificial Sequence

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APPLICANT: Restoragen Inc.
APPLICANT: Seo, Jin Seog
APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Holmquist, Barton
TITLE OF INVENTION: Polypeptide Cleavage Process
FILE REPERENCE: 1627.026401
FURRENT FILING DATE: 2003.05-23
PRIOR APPLICATION NUMBER: US 60/383,488
PRIOR PLICATION NUMBER: 2002-05-24
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
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72.0%; Score 18; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0;
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APPLICANT: Strydom, Daniel
APPLICANT: Strydom, Daniel
APPLICANT: Crydom, Daniel
APPLICANT: Crydom, Daniel
APPLICANT: Crydom, Peptide Amidation Process
TITLE OF INVENTION: Peptide Amidation Process
FILE REFERENCE: 1627.012401
CURRENT APPLICATION NUMBER: DCT/US03/16648A
CURRENT FILING DATE: 2003-05-23
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 43
SOFWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Artificial Construct PCT-US03-16468A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: A synthetic peptide PCT-US03-16648A-39
                                                                                                                                                              Sequence 13, Application PC/TUS0316468A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application PC/TUS0316648A GENERAL INFORMATION:
APPLICANT: Restoragen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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PCT-US03-16648A-39
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LENGTH: 4
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-09-657-276-1153.
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GENERAL INFORMATION:
APPLICANT: Thackur, Madhukar (Matthew) L.
FYDILGANT: Thackur, Madhukar (Matthew) L.
TITLE OF INVENTION: Imaging with TC-99m Labeled Fibrin Alpha
FILE REPRENCE: 8321-119
CURRENT APPLICATION NUMBER: US/09/763,777B
CURRENT FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: PCT/US99/19011
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PASECED for Windows Version 4.0
SEQ ID NO 1
FEAST DATE: 1998-08-17
SEQ ID NO 1
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PCT-US03-08732-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.0%; Score 18; DB 22; Length 3; ilarity 100.0%; Pred. No. 5.5e+06; Conservative 0; Mismatches 0; Indels
                                                                                              Length 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: N-terminus tripeptide portion of ; OTHER INFORMATION: fibrin-alpha-chain peptide US-09-763-777B-1
                                                                                           DB 20; L
5.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS0308732
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
THE OF INFURITION:
FILLE OF INFURITION:
FILLE OF INFURITION:
CURRENT APPLICATION NUMBER: PCT/US03/08732
CURRENT APPLICATION NUMBER: US 60/367,645
PRIOR FILING DATE: 2002-03-26
                                                                                           h 72.0%; Score 18; DB Similarity 100.0%; Pred. No. 5.5 3; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
                                                                                         Query Match
Best Local Similarity
Matches 3; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: artificial
                                                                                                                                                                                       1 GPR 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GPR 3
                                                                                                                                                                                                                                                                                                      RESULT 41
US-09-763-777B-1
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Gaps
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                                          0; Indels
Query Match 72.0%; Score 18; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 3; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12974A
FILING DATE: 23 Jul 97
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35, Application PC/TUS9719557
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19557
FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
72.0%; Score 18; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/685,589
FILING DATE: 24-JUL-1996
ATTORNEY/AGENT INPORMATION:
NAME: COTUZZI, LAULA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELEPHONE: 212-790-9990
TELEPAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.4

OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-12974A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: unknown TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: not relevan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US97-19557-35
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GENERAL INFORMATION:
GENERAL INFORMATION:
CHANG: Change Conway
APPLICANT: Chan, Jie
APPLICANT: Chen, Jie
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
                             Sequence 35, Application PC/TUS9712974A
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOFPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12974A
FILING DATE: 23 Jul 97
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%; Score 18; DB 1; L
100.0%; Pred. No. 5.5e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
| LOCATION: 1..4
| COTHEN TINCPRATION: /product= "Beta-turn"
PCT-US97-12974A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/685,589
FILING DATE: 24-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: COFFUZZI, LAUKE A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-228
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-9741
                                                                                                                                                                                                                                                  ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 And CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GPR 3
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PCT-US97-12974A-36
                 PCT-US97-12974A-35
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APPLICANT: ROBERT F. Hird, Edward F. Cosgrove
TITLE OF INVENTION: Test Kits and Methods for Rapidly
TITLE OF INVENTION: Test Kits and Methods for Rapidly
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hird and Cosgrove
STREET: 1110 Burnett Avenue, Suite D
CITY: Concord
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Inaging
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
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    Length 4;
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IDENTIFICATION METHOD: Similarity to other signal IDENTIFICATION METHOD: sequences, hydrophobic OTHER INFORMATION: Xaa in location 1 of following OTHER INFORMATION: sequence is Tosyl
72.0%; Score 18; DB 1; Lo
ilarity 100.0%; Pred. No. 5.5e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
72.0%; Score 18; DB 4; Le Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: MD2-HD, DS/HD, 1.2 MB
CORPUTER: Memorex Telex
OPERATING SYSTEM: MS-DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,621
FILING DATE: 25-March, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
NAME: APPLICATION DATA: None
ATTORNEY/AGENT INFORMATION:
NAME: APPLICATION DATA: 15612-3
TELECOMMUNICATION INFORMATION:
TELEFRONE: ($10) 676-2733
TELEFRONE: ($10) 676-2734
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE: CARRACTERISTICS:
                                                                                                                                                                                                                                 Sequence 4, Application US/08037621 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Protein
FEATURE:
NAME/KEY: Signal Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 4 Amino Acids
Amino Acid
SY: Linear
      Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                      JS-08-037-621-4
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.0%; Score 18; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US97-19557-36

Sequence 36, Application PC/TUS9719557

APPLICANT: Chang, Conway

APPLICANT: Chang, Loo

APPLICANT: Chen, Jie

TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD

NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds LLP

STREET: LIS5 Avenue of the Americas

CITY: New York

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19557 FILING DATE: herewith CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide

LOCATION: 1..4

OTHER INFORMATION: /product= "Beta-turn"

PCT-US97-19557-36
                                                                                                                                                                                                                                                                                                           LOCATION: 1.4

OTHER INFORMATION: /product= "Beta-turn"

PCT-US97-19557-35
           8067-048-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: COCUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 6067-048-228
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212-79-9990
TELEPRAX: 212-789-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INPORMATION:
TELEPRONE: 212-790-9090
TELEPRX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                            TYPE: amino acids
STRANDEDNESS: unknown
TOPOLGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
                                                                                            TELEX: 66141
INPORMATION FOR SEQ ID NO:
SEQUENCTION FOR SEQUENCE:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: unknown
not relevant
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                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPR 3
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Gaps

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Query Match 72.0%; Score 18; DB 6; Length 4; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 3; Conservative 0; Mismatches 0; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
GTTY: Chicago
STATE: 111nois
COUNTY: USA
ZIP: 60606
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYTEM: PC-DoS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/653,012
FILING DATE: 22-UN-1994
CLASSIFICATION NUMBER: US 07/653,012
FILING DATE: 08-FEB-1991
APPLICATION NUMBER: 26,949
FRIENCA REPERTY NUMBER: 26,949
FRIEDROME MCDonnell, John U REGISTRATION NUMBER: 90,1104
TELECOMMUNICATION INFORMATION:
TELECHOME: 312 715 1030
TELECHOME: 312 715 1234
TELECOMMUNICATION INFORMATION:
TELECHOME: 312 715 1234
TELECHOME: 312 715 1234
TELECHOME: A mino acids
TUPORATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 mino acid
TUPOLOGY: 1 linear
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Search completed: September 7, 2004, 19:32:29 Job time : 406 secs

1 GPR 3

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16, Appl 3561, Ap 3561, Ap 3562, Appl 224, Appl 81, Appl 171, Appl

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

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Sequence 4, Appli
Sequence 5, Appli
Sequence 62, Appli
Sequence 90, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 158, Appli
Sequence 25, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
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                                                                                                2004, 19:24:42; Search time 59 Seconds (without alignments) 8.769 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pending Patents AA New:*

1: /cgn2 6/ptodata/2/paa/PCT NEW COMB.pep:*

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4: /cgn2_6/ptodata/2/paa/US07_NEW COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW COMB.pep:*

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7: /cgn2_6/ptodata/2/paa/US08_NEW COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US06_NEW COMB.pep:*
                                                                                                                                                                                                                                                                                                     6105
              GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US04-16828-4
PCT-US04-16828-4
PCT-US04-16828-4
PCT-US04-16828-4
US-10-489-804-331
US-10-459-804-7328-24
US-10-459-0308-2
US-10-459-0308-4
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US-10-459-0308-4
US-10-720-831-5
US-60-548-401-3581
PCT-US04-11167-158
US-60-548-401-3586
                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries
                                                                        using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                      OM protein - protein search,
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                                                                                                                                                                                                                                                                                                                                 length: 0
length: 4
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Maximum DB seq
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Perfect
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No.
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Sequence

ALIGNMENTS

IIC STEM		Gaps 0;
ULT 1	FERTURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: polypeptide USO4-10121-1	Length 4; 5; Indels 0;
UNT 1 -USO4-10121-1 -USO4-10121-1 -USO4-10121-1 -USO4-10121-1 -USO4-10121-1 -USO4-10121-1 -USO4-10121-1 -USO4-10121-1 -USO4-1012-1 -USO4-1013-1 -USOF-10-1 -USOF-10-1 -USOF-10-1 -USOF-10-1 -USO4-10-1 -USO4-1 -USO4-10-1 -USO4-1 -USO	of Artificial Sec	100.0%; Score 25; DB 1; Length 4; 100.0%; Pred. No. 6.2e+05; ative 0; Mismatches 0; Indels
SULT 1 T-GS04-10121-1 GENERAL INFORMATION GENERAL INFORMATION: APPLICANT: BRESAGEN INC. APPLICANT: BRESAGEN INC. APPLICANT: WIVERSITY OF GEORGIA RESEARCH TITLE OF INVENTION: METHODS FOR NEURAL DIF TITLE OF INVENTION: CELLES USING PROTEASE TITLE OF INVENTION: CELLES USING PROTEASE TITLE OF INVENTION: CELLES USING PROTEASE CURRENT APPLICATION NUMBER: PCT/USO4/10121 CURRENT FILING DATE: 2004-03-31 NUMBER OF SEQ ID NOS: 5 SOFTWARE: Patentin Ver: 3.2 SEQ ID NO 1 LENGTH: 4 TYPE: PRT CREANISM: Artificial Sequence	FEATURE: OTHER INFORMATION: Description (OTHER INFORMATION: polypeptide USO4-10121-1	
RESULT 1 PCT-USO4-10121-1 PCT-USO4-10121-1 GENERAL INFORMATION: APPLICANT: BRESAGEN INC. APPLICANT: WINVERSITY OF GEO TITLE OF INVENTION: METHODS F: TITLE OF INVENTION: CELLS US; TITLE OF INVENTION: CELLS US; TITLE OF INVENTION: CELLS US; TITLE OF INVENTION: METHODS F: TITLE OF INVENTION: CELLS US; TITLE OF INVENTION OUMBER: PARIOR PELICATION NUMBER: 60, PRIOR FILING DATE: 2003-03-31 SOFTWARE: PATENTING DATE: 2003-03-31 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PATENTING OFF: 3.2 SOFTWARE: PATENTING OFF: 3.2 SOFTWARE: PATENTING OFF: 3.2 SEQ ID NO 1 LENGTH: ATTYPE: PRT TYPE: PRT TYPE: PRT	; FEATURE: ; OTHER INFORMATIC ; OTHER INFORMATIC PCT-US04-10121-1	Query Match Best Local Similarity Matches 4; Conserv

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APPLICANT: OREGON HEALTH AND SCIENCE UNIVERSITY APPLICANT: COWLEY, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Polypeptide variation
US-10-489-804-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-459-030B-2
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PCT-US03-40762-1
Sequence 1, Application PC/TUS0340762
GENERAL INFORMATION:
PAPPLICANT: BRESAGEN, INC.
APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
APPLICANT: OF INVENTION: STABLILIZATION
TITLE OF INVENTION: STABLILIZATION
FILE REFERENCE: 18377-0028
CURRENT PAPLICATION NUMBER: PCT/US03/40762
CURRENT PAPLICATION NUMBER: PCT/US03/40762
PRIOR APPLICATION NUMBER: 60/434,786
PRIOR APPLICATION NUMBER: 60/434,786
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN OF: 3.2
SEQ ID NO 1
LENGTH: 4
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence; Note; OTHER INFORMATION: synthetic construct
PCT-USO4-16828-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                 APPLICANT: University of Texas
TITLE OF INVENTION: Micropositioning Cells for Tissue
TITLE OF INVENTION: Micropositioning Cells for Tissue
FITE REPERENCE: 21105.0003P1
CURRENT APPLICATION NUMBER: PCT/US04/16828
CURRENT FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: 60/474,574
PROR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 4
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Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                      Sequence 4, Application PC/TUS0416828
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 4; Conserv
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APPLICANT: Cone, Roger
APPLICANT: Low, Malcolm
APPLICANT: Buller. Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Screen for Agents
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Screen for Agents
FILE REPRENCE: 899-68036
CURRENT APPLICATION NUMBER: US/10/489,804
CURRENT FILING DATE: 2004-03-16
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 352
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
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; OTHER INFORMATION: Amino acid sequence of a cleavage sequence for thrombin
US-10-477-712B-62
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL PEtzelbauer, Peter
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REPERBNCE A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US(10/459,030B
CURRENT FILING DATE: 2003-06-11
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10-477-712B-62

| Sequence 62, Application US/10477712B
| Sequence 62, Application US/10477712B
| GENERAL INFORMATION:
| APPLICANT: Takeda Chemical Industries, Ltd.
| TITLE OF INVENTION: A Method for Producing A Peptide
| FILE REFERENCE: OKA-0213
| CURRENT APPLICATION NUMBER: US/10/477,712B
| PRIOR FILING DATE: 2003-11-14
| PRIOR FILING DATE: 2001-05-17
| NUMBER: OF SEQ ID NOS: 85
| SEQ ID NO 62
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                                                                                                                                                                                                                                                               SEQUENCE 4, Application US/10459030B
SEQUENCE 1 INFORMATION:
APPLICANT: Petzelbauer, Peter
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR APPLICATION NUMBER: AT 2063/2000
SPIGNARE OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
                                                   Gaps
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                                                0; Indels
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     Length 4;
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OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: sptrembl/Q9UCG8/Q9UCG8
US-10-821-240A-151
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72.0%; Score 18; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 3; Conservative 0; Mismatches 0;
  Score 18; DB 5; Lu
Pred. No. 6.2e+05;
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Sequence 151, Application US/10821240A
GENERAL INFORMATION:
APPLICANT: Khan, Nisar A.
APPLICANT: Reans, Nisar A.
APPLICANT: Benner, Robert
TITLE OF INVENTION: Gene regulator
FILE REFERENCE: 2183-22330
CURRENT PELING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: US/10/821,240A
CURRENT PILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 312
SEQ ID NOS: 312
SEQ ID NO 151
                                                     0; Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptide of formula I
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LOCATION: 4
CTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-4
     72.0%; 8
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ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 100.
Matches 3; Conservative
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US-10-821-240A-151
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OTHER INFORMATION: mammalian, peptide specifically cleavable by a reagent produced
OTHER INFORMATION: a target cell
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ITILE OF INVENTION: RECOMBINANT PROTEINS CONTAINING REPEATING UNITS
FILE REPEARNCE: MONS:016US
CURRENT APPLICATION NUMBER: US/09/804,733E
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/188,990
PRIOR APPLICATION NUMBER: 60/188,990
PRIOR FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 24
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GENERAL INFORMATION:
APPLICANT: Lauermann, Vit
TITLE OF INVENTION: Targeted release
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/651,584C
CURRENT FILING DATE: 2003-08-30
NUMBER OF SEQ ID NOS: 111
SENGTH: 3
LENGTH: 3
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: AT 2063/2000
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3
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; OTHER INFORMATION: peptide of formula I
US-10-459-030B-2
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US-09-804-733E-24
; Sequence 24, Application US/09804733E
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 3; Conservative
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ORGANISM: Unknown
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Query Match 68.0%; Score 17; DB 7; I Best Local Similarity 75.0%; Pred. No. 6.2e+05; Matches 3; Conservative 0; Mismatches 1;
                                                         FEATURE:
, OTHER INFORMATION: Synthetic peptide
US-60-548-401-3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application PC/TUS0340762 GENERAL INFORMATION:
                   TYPE: PRT
ORGANISM: Artificial sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SOFWARE: Patentin Ver. 3.2
SEQ ID NO 4
LENGTH: 4
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LENGTH: 4
LENGIH: 4
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GRNERAL INFORMATION:
APPLICANT: Sidelman, Zvi
TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
FILE REPRENDENCE: 27567
CURRENT APPLICATION NUMBER: US/60/548,401
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 3581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/720,831
FILING DATE: 24-Nov-2003
CLASSIFICATION: 435
                                                                                                                                                                                                                        Wallace, Donald
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: COLLAGEN CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/278,774
FILING DATE: 22-UUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Rafayko, Kathi L
REGISTRATION NUMBER: 36,644
REFERENCE/DOCKET NUMBER: 94-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-4642
TELEFAX: (415) 354-4752
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: COLLAGEN CORPORATION STREET: 2500 Faber Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-720-831-5
                                                                                                                                                          Sequence 5, Application US/10720831 GENERAL INFORMATION:
                                                                                                                                                                                                    APPLICANT: Berg, Richard A
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: California
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US-10-720-831-5
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RESULT 13
PCT-USO4-10121-4
; Sequence 4, Application PC/TUS0410121
; GENERAL INFORMATION:
; APPLICANT: BRESAGEN INC.
; APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
; TITLE OF INVENTION: METHODS FOR NBURAL DIFFERENTIATION OF EMBRYONIC STEM
; TITLE OF INVENTION: CELLS USING PROTEASE PASSAGING TECHNIQUES
; FILE REPREMENT
; CURRENT PILING DATE: 2004-03-31
; CURRENT FILING DATE: 2004-03-31
; FRICA APPLICATION NUMBER: 60/459,090
; PRIOR PILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATCHIN VET. 3.2
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APPLICANT: BRESGAGEN, INC.
APPLICANT: BRESGAGEN, INC.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL CELL PRODUCTION AND
TITLE OF INVENTION: STABILIZATION
FILE REFERENCE: 18377-0028
CURRENT APPLICATION NUMBER: PCT/US03/40762
CURRENT FILING DATE: 2003-112-18
PRIOR APPLICATION NUMBER: 60/434,786
PRIOR FILING DATE: 2002-12-18
                                                            Gaps
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
PCT-US03-40762-4
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Length 4;
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us-09-931-009a-2.closed.rapn

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TYPE: PRT
ORGANISM: BOVINE
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                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Harris, Jennifer L.
APPLICANT: Backes, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: Ellman, Jonathan A.
APPLICANT: Ellman, Jonathan A.
APPLICANT: Ellman, Jonathan A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Profiling of Protease Specificity Using Combinatorial
TITLE OF INVENTION: Profiling of Protease Specificity Using Combinatorial
TITLE OF INVENTION: Profiling of Protease Specificity Using Combinatorial
TITLE OF INVENTION: Profiling of Protease Specificity Using Combinatorial
TITLE OF INVENTION: Profiling of Protease Specificity Using Combinatorial
FILE REFERENCE: 180626-0032110S
CURRENT APPLICATION NUMBER: US 60/209,274
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/209,274
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: WO PCT/US01/17265
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: WO PCT/US01/17265
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: WO PCT/US01/17265
PRIOR FILING DATE: 2001-05-25

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Best Local Similarity 66.7%; Pred. No. 6.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels
Score 16; DB 1; Length 4; Pred. No. 6.2e+05; 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/10686884 GENERAL INFORMATION:
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Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
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APPLICANT: GILCHRIST,
APPLICANT: GILCHRIST,
APPLICANT: HAWA, HEIDI
APPLICANT: HAWA, HEIDI
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: METHOD
FILE REPRENCE: 2661-102
CURRENT PAPLICATION NUMBER: DCT/USO4/11167
CURRENT PLING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 10/411336
PRIOR APPLICATION NUMBER: US 09/852910
PRIOR APPLICATION NUMBER: US 00/852910
PRIOR PILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PALENTH VETSION 3.2
SEQ ID NO 158
INNOVAL DATE: DATE NOTE: DATE 
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Pred. No. 6.2e+05;
1; Mismatches 0; Indels
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Pred. No. 6.2e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CT-US04-11167-158
Sequence 158, Application PC/TUS0411167
GENERAL INFORMATION:
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US-09-852-910B-158
; Sequence 158, Application US/09852910B
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Best Local Similarity 66.7%;
Matches 2; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 2; Conservative
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Gaps

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Sequence 519, Application US/60548401
GENERAL INFORMATION:
APPLICANT: Sidelman, Zvi
TITLE OF INVENTION: CASEIN DERIVED FEPTIDES AND USES THEREOF IN SARS THERAPY
FILE REFERENCE: 27567
CURRENT APPLICATION NUMBER: US/60/548,401
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sidelman, Zvi
TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
FILE REPERENCE: 2756.
CURRENT APPLICATION NUMBER: US/60/548,401
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: Patentin version 3.2
SEQ ID NO 3546
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                                                                                                                Score 14; DB 7; Length 4; Pred. No. 6.2e+05; 0; Mismatches 1; Indels
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                                             ; OTHER INFORMATION: Synthetic peptide US-60-548-401-518
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OTHER INFORMATION: Synthetic peptide

US-60-548-401-519
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FEATURE:
OTHER INFORMATION: Synthetic peptide
US-60-548-401-3546
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; Sequence 3550, Application US/60548401
    ORGANISM: Artificial sequence
                                                                                                                Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
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              APPLICANT: GILCHRIST, ANNETTE
APPLICANT: GILCHRIST, ANNETTE
APPLICANT: GILCHRIST, ANNETTE
APPLICANT: GILCHRIST, HANN, HEIDI
TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
TITLE OF INVENTION: MATHER, 108
FILLS REFRENCE: 2661-101
CURRENT APPLICATION WUMBER: US 60/275472
PRIOR APPLICATION WUMBER: US 60/275472
NUMBER OF SEQ ID NOS: 271
SSOFTWARE: Patentin version 3.2
LENGTH: 4
LENGTH: 4
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
FILE REFERENCE: 27567
CURRENT APPLICATION NUMBER: US/60/548,401
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: Patentin version 3.2
SEQ ID NO 518
LENGTH: 4
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Health Marrix Sciences
APPLICANT: Mitts, Thomas
APPLICANT: Jimenez, Felipe
TITLE OF INVENTION: ELASTIN DIGEST COMPOSITIONS AND METHODS UTLLIZING SAME
FILE REPERENCE: 126595,101
CURRENT APPLICATION NUMBER: US/10/778,253
FROR APPLICATION NUMBER: 60/447461
PRIOR FILING DATE: 2003-02-14
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Pred. No. 6.2e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID, NOS: 44
SOFTWARE: PatentIn version 3.2
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Best Local Similarity 66,7'
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
GENERAL INFORMATION:
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; ORGANISM: BOVINE
US-10-778-253-36
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US-60-548-401-518
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US-10-778-253-36
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Gaps

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Gaps

Gaps

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) ORGANISM: Artificial Sequence

) FEATURE:

) OTHER INFORMATION: Synthetic example of peptide modulator of P2Y2 or P2Y1 receptors

PCT-US03-33658A-26
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GENERAL INFORMATION:
APPLICANT: Alibhai, Murtaza
APPLICANT: Alibhai, Murtaza
APPLICANT: Alibhai, Murtaza
APPLICANT: Alibhai, Murtaza
TITLE OF INVENTION: Insect Inhibitory Lipid Acyl Hydrolases
TILE REPERENCE: 38-21 (51842)B
CURRENT APPLICATION NUMBER: US/10/682,011
CURRENT FILING DATE: 2003-10-09
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE PATENTIN VERSION 3.0
SEQ ID NO 16
LENGTH: 3
LENGTH: 3
LENGTH: 3
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                                                                                                                 Query Match
52.0%; Score 13; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0;
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ORGANISM: synthetic
PEATURE:
NAME/KEY: Protein
LOCATION: (1)..(3)
COTHER INFORMATION: Linker Sequence
US-10-682-011-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 2; Conservative
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1 GP 2
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                                  APPLICANT: Sidelman, Zvi
TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
FILE REPERENCE: 27567
CURRENT APPLICATION NUMBER: US/60/548,401
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: Patentin version 3.2
SEQ ID NO 3550
LENGTH: 2
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APPLICANT: Villanueva, Julie M.
APPLICANT: Quirk, Stephen
APPLICANT: Stuberly-Clark worldwide, Inc.
TITLE OF INVENTION: Compounds that Bind P2Y2 or P2Y1 Receptors
FILE REFRENCE: 1443.029W01
CURRENT APPLICATION NUMBER: PCT/US03/33658A
CURRENT PILING DATE: 2003-10-22
PRIOR FILING DATE: 2003-10-22
PRIOR FILING DATE: 2002-12-16
NUMBER OF SEQ 1D NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PASTSEQ for Windows PASSON 1.
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Sequence 70, Application PC/TUSO402004
GENERAL INFORMATION:
APPLICANT: Eli Lilly and Company
TITLE OF INVENTION: Abeta Binding Molecules
FILE REPERENCE: X-16068
CURRENT APPLICATION NUMBER: PCT/USO4/02004
CURRENT FILING DATE: 2004-02-06
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.2
SECTURENT: 3
LENGTH: 3
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PCT-US03-33658A-26
; Sequence 26, Application PC/TUS0333658A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: Synthetic peptide US-60-548-401-3550
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                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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ORGANISM: Artificial sequence
FEATURE:
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52.0%; Score 13; DB 1; Length 4;
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S-60-548-401-3562
Sequence 3562, Application US/60548401
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
FILE REPERENCE: 27567
CURRENT APPLICATION NUMBER: US/60/548,401
CURRENT PILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sidelman, Zvi
TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
FILE REFERENCE: 2756,
CURRENT APPLICATION NUMBER: US/60/548,401
CURRENT APPLICATION NUMBER: 2004-03-01
NUMBER OF SEQ ID NOS: 4000
SOFTWARE: PATENTIN VERSION 3.2
LENGTH: 3
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Sequence 3566, Application US/60548401

GENERAL INFORMATION:
APPLICANT: SideJanan, Zvi

TITLE OF INVENTION: CASEIN DERIVED PEPTIDES AND USES THEREOF IN SARS THERAPY
FILE REPERENCE: 27567

CURRENT APPLICATION UNMERR: US/60/548,401

CURRENT FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 4000

SOFTWARE: PATENTIN VERSION 3.2

SOFTWARE: PATENTIN VERSION 3.2

LENGTH: 3
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                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic peptide US-60-548-401-3562
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 2; Conservative
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RESULT 32
PCT-US03-35056-224
; Sequence 224, Application PC/TUS0335026
; GENERAL INFORMATION:
    APPLICANT: Rainin, Sen
; APPLICANT: Maiphin, Sen
; APPLICANT: Corr, Maiphin A.
    APPLICANT: Maiphin A.
    APP
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PCT-USG4-04137-26

Sequence 26. Application PC/TUS0404137

Sequence 26. Application PC/TUS0404137

Seguence 26. Application PC/TUS0404137

APPLICANT: Health Matrix Sciences

APPLICANT: Mitts, Thomas

APPLICANT: Jimenea, Felipe

TITLE OF INVENTION: ELASTIN DIGEST COMPOSITIONS AND METHODS UTILIZING SAME
FILE REPRENCE: 125695.102

CURRENT APPLICATION NUMBER: PCT/US04/04137

CURRENT PILING DATE: 2004-02-13

PRIOR APPLICATION UNMBER: 60447461

PRIOR APPLICATION UNMBER: 60447461

SOUTHWARE: PAGE IN NOS: 44

SOUTHWARE: PAGE IN NOS: 44
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PCT-US03-35026-224
                                                                                                                                                                                                                                                                                                                                         ;
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; FEATURE:
; CTHER INFORMATION: Synthetic peptide
US-60-548-401-3566
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 224
LENGTH: 4
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GILCHRIST, ANNETTE
APPLICANT: GILCHRIST, ANNETTE
TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
TITLE OF INVENTION: SIGNALING
FILE REPERENCE: 2661-102
CURRENT FILING DATE: 2004-04-16
PRIOR PAPLICATION NUMBER: US 10/411336
PRIOR PLING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 09/852910
PRIOR APPLICATION NUMBER: US 09/852910
PRIOR PLING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/275472
PRIOR PLING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PALENTIN VERSION 3.2
SEQ ID NO 11
LENGTH: 4
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APPLICANT: TRANSGENES, LLC
APPLICANT: The Board of Supervisors of Louisiana State University and
APPLICANT: The Board of Supervisors of Louisiana State University and
APPLICANT: Agricultural and Mechanical College
TITLE OF INVENTION: Production of Multimeric Proteins
FILE REFERENCE: 51687-0230WP (51687-295696)
CURRENT PAPLICATION NUMBER: PC1/0503/41261
PRIOR FILING DATE: 2003-10-21
PRIOR APPLICATION NUMBER: US 60/441,405
PRIOR FILING DATE: 2003-01-21
PRIOR FILING DATE: 2003-01-21
PRIOR FILING DATE: 2003-01-21
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SOFTWARE: Patentin version 3.2
SEQ ID NO 81
      Query Match 52.0
Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                        1 GP 2
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APPLICANT: Jimenez, Felipe
TITLE OF INVENTIONS ELASTIN DIGEST COMPOSITIONS AND METHODS UTILIZING SAME
FILE REPERENCE: 126595,102
CURRENT APPLICATION NUMBER: PCT/US04/04137
CURRENT APPLICATION NUMBER: PCT/US04/04137
PRIOR APPLICATION NUMBER: 60/447461
PRIOR PILING DATE: 2003-02-14
NUMBER OF SED ID NOS: 44
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 4
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GENERAL INFORMATION:
APPLICANT: TRANSGENES, LLC
APPLICANT: TRANSGENES, LLC
APPLICANT: TRANSGENES, LLC
APPLICANT: TRANSGENES, LLC
APPLICANT: Agricultural and Mechanical College
TITLE OF INVENTION: Vaccine Production Using Transposon Based Vectors
TITLE OF INVENTION: Vaccine Production Using Transposon Based Vectors
FILE REFRENCE: 51687-0270WP (61687-29581)
CURRENT APPLICATION NUMBER: PCT/US03/41269
CURRENT PRING DATE: 2003-10-24
FRIOR FILING DATE: 2003-01-21
                                             Gaps
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                                      Indels
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Best Local Similarity 100.0%; Pred. No. 6.2e+05; Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           CT-US04-04137-28
Sequence 28, Application PC/TUS0404137
SepureRAL INPERMATION:
APPLICANT: Health Matrix Sciences
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SOFTWARE: Patentin version 3.2
SEQ ID NO 81
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Best Local Similarity
Matches 2; Conserv
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SEQUENCE 171, Application US/09852910B
SEQUENCE 171, Application US/09852910B
SEQUENCE 171, ADDITORNATION:
APPLICANT: GILCHRIST, ANNETTE
APPLICANT: GILCHRIST, ANNETTE
APPLICANT: HAMM, HEIDI
TITLE OF INVENTION: SIGNALING
FILE REPERENCE: 2661-101
CURRENT APPLICATION NUMBER: US/09/852,910B
CURRENT PILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/275472
PRIOR APPLICATION NUMBER: US 60/275472
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PATENTIN VEERION 3.2
SEQ ID NO 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 2, Application PC/TUS0340762
SEQUENCE 2, Application PC/TUS0340762
SEQUENCE 2, APPLICANT: BRESAGEN, INC.
APPLICANT: BRESAGEN, INC.
APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
TITLE OF INVENTION: STABLILIZATION
FILE REFERENCE: 18377-0028
FILE REFERENCE: 18377-0028
CURRENT APPLICATION NUMBER: PCT/US03/40762
CURRENT PILING DATE: 2003-12-18
PRIOR APPLICATION NUMBER: 60/434,786
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 2
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                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: polypeptide
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100.0%; Pred. No. 6.2e+05;
tive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 2
LENGTH: 4
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Best Local Similarity 100.
Matches 2; Conservative
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-US03-40762-2
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APPLICANT: TRANSCENRES, LLC
APPLICANT: TRANSCENRES, LLC
APPLICANT: TRANSCENRES, LLC
APPLICANT: The Board of Supervisors fo Louisiana State University and
APPLICANT: The Board of Supervisors fo Louisiana State University and
APPLICANT: Agricultural and Mechanical College
AITLE OF INVENTION: Administration of Transposon-Based Vectors to Reproductive Organs
FILE REFERENCE: 51697-0280WP (51687-295699)
CURRENT APPLICATION NUMBER: US 60/441,381
PRIOR PILING DATE: 2003-10-21
PRIOR PELICATION NUMBER: US 60/441,405
PRIOR FILING DATE: 2003-01-21
PRIOR PRIOR APPLICATION NUMBER: US 60/441,502
PRIOR APPLICATION NUMBER: US 60/441,392
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BRESAGEN INC.
APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
APPLICANT: UNIVERSITY OF GELES USING PROTEASE PASSAGING TECHNIQUES
TITLE OF INVENTION: GELES USING PROTEASE PASSAGING TECHNIQUES
FILE REFERENCE: 18377-0031
CURRENT APPLICATION NUMBER: PCT/US04/10121
PRIOR APPLICATION NUMBER: 60/459,090
PRIOR FILING DATE: 2003-03-31
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PRIOR APPLICATION NUMBER: US 60/441,377
PRIOR PILING DATE: 2003-01-21
PRIOR PILING DATE: 2003-01-21
PRIOR FILING DATE: 2003-06-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.2
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26, Application PC/TUS0341335 GENERAL INFORMATION:
     LENGTH: 4
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
PETATURE:
OTHER INFORMATION: Synthetic
PCT-US03-41261-81
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Best Local Similarity 100.
Matches 2; Conservative
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1 GP 2
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                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MUNDAY, Gregory
APPLICANT: Research, I. Ross
APPLICANT: Rossini, G.
ITLE OF INVENTION: STIMULATING BONE AND HAIR GROWTH
TITLE OF INVENTION: STIMULATING BONE AND HAIR GROWTH
FILE REFERENCE: 43722200562
CURRENT APPLICATION NUMBER: US/09/558,973
CURRENT PLING DATE: 2000-04-25
PRIOR PLING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Garrett, I. Ross
APPLICANT: Garrett, I. Ross
APPLICANT: Rossini, Gregory
APPLICANT: Rossini, Gregory
TITLE OF INVENTION: INHIBITORS OF PROTEASONAL ACTIVITY FOR
TITLE OF INVENTION: STIMULATING BONE AND HAIR GROWTH
FILE REPREMENT 3222002622
CURRENT APPLICATION NUMBER: US 09/421,545
PRIOR APPLICATION NUMBER: US 09/421,545
PRIOR APPLICATION NUMBER: US 09/361,775
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1998-07-10
NUMBER OF FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
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52.0%; Score 13; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                     Length 4;
                                                   52.0%; Score 13; DB 5; Le
100.0%; Pred. No. 6.2e+05;
tive 0; Mismatches 0;
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US-09-558-973-2
; Sequence 2, Application US/09558973
; GENERAL INFORMATION:
                                                Query Match
Best Local Similarity 100.
Matches 2; Conservative
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ORGANISM: Unknown
FEATURE:
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     US-09-421-545-2
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US-09-558-973-1
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ORGANISM: Unknown
FEBATURE:
OTHER INFORMATION: a.a. portion of ALLM compound as proteasome
OTHER INFORMATION: inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: a.a. portion of ALLM compound as proteasome OTHER INFORMATION: inhibitor
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Sequence 2, Application US/09421545

Sequence 2, Application US/09421545

Sequence 2, Application US/09421545

GENERAL INFORMATION:

APPLICANT: Mundy, Gregory

APPLICANT: Garrett, I. Ross

APPLICANT: Rossini, G.

ITLE OF INVENTION: INHIBITORS OF PROTEASOMAL ACTIVITY FOR TILE OF INVENTION: INHIBITORS OF PROTEASOMAL ACTIVITY FOR TILE OF INVENTION: STIMOLATING BONE AND HAIR GROWTH

FILE REFERRING: 1999-10-20

CURRENT PLILING DATE: 1999-07-27

PRIOR FILING DATE: 1999-07-27

PRIOR FILING DATE: 1999-07-10

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 4

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US-09-421-545-1
; Sequence 1, Application US/09421545
; GENERAL INFORMATION:
; APPLICANT: Mundy, Gregory
; APPLICANT: Restini, G.
; TITLE OF INVENTION: INHIBITORS OF PROTEASOWAL ACTIVITY FOR
; TITLE OF INVENTION: STIMULATING BONE AND HAIR GROWTH
; FILE REFERENCE: 432722002621
; CURRENT APPLICATION NUMBER: US/09/421,545
; CURRENT FILING DATE: 1999-10-20
; PRIOR PRILICATION NUMBER: 09/361,775
; PRIOR FILING DATE: 1999-07-27
; PRIOR FILING DATE: 1999-07-27
; WUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                       1; Indels
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                                                                            Length 4;
; OTHER INFORMATION: G alpha 11 library linker sequence US-09-852-910B-171
                                                                       Score 13; DB 5; I
Pred. No. 6.2e+05;
0; Mismatches 1,
                                                                    Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
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ORGANISM: Unknown
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Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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ORGANISM: Unknown
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ORGANISM: Unknown
                                                                                                               1 GP 2
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US-09-695-807-1
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                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Novel Compositions and Methods of Screening for T-Cell TITLE OF INVENTION: Novel Compositions and Methods of Screening for T-Cell FILE OF INVENTION: and B-Cell Activation Modulators FILE REPRENCE: 021044-00571005 CURRENT PRILING DATE: 1999-10-28 PRIOR PILING DATE: 1999-10-28 PRIOR PILING DATE: 1998-10-28 NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 18
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OTHER INFORMATION: a.a. portion of ALLM compound as proteasome; OTHER INFORMATION: inhibitor
US-09-558-973-2
                                                                                                               Query Match 52.0%; Score 13; DB 5; Length 4; Best Local Similarity 100.0%; Pred. No. 6.2e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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APPLICANT: Lamb, Jonathan R
APPLICANT: Lamb, Margaret J
APPLICANT: Dallman, Margaret J
APPLICANT: Dallman, Margaret J
APPLICANT: Dallman, Margaret J
CURRENT SPILICATION NUMBER: US/09/310,685
CURRENT APPLICATION NUMBER: US/09/310,685
CURRENT FILING DATE: 1999-05-04
PRIOR FILING DATE: 1996-11-07
PRIOR PILING DATE: 1996-11
PRIOR PILING DATE: 1997-07-24
PRIOR PILING DATE: 1997-07-24
PRIOR PILING DATE: 1997-07-11
PRIOR FILING DATE: 1997-09-11
PRIOR FILING DATE: 1997-09-11
PRIOR FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Version 3.2
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/09310685 GENERAL INFORMATION:
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FEATURE:
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US-09-310-685-23
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Base Local Similarity 100.0%; Pred, No. 6.24-05; Amatches 2; Conservative 0, Mismatches 0; Indels 0, Gaps 0, 10P 2

Deer 10P 2

Deer Similarity 100.0%; Pred, No. 6.24-05; Amatches 2; Conservative 0, Mismatches 0; Indels 0, Gaps 10P 2

Deer 10P 2

US-05-65-80-1

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US-09-590-6550-48

J Sequence 48, Application US/09592695D

Sequence 48, Application US/09592695D

Sequence 48, Application

APPLICANT: Cochran, Andrea G.

APPLICANT: Starovasnik, Melbasa A.

TITLE OF INVENITON: Libraries On Phage

TITLE OF INVENITON: Libraries On Phage

TITLE OF INVENITON: Libraries On Phage

FILE REPERBRCE: 11669.116091

CURRENT FILING DATE: 2000-06-13

PRIOR APPLICATION NUMBER: US 60/139,017

NUMBER OF SEQ ID NOS: 49

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FRATURES

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                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                           0;
; OTHER INFORMATION: a.a. portion of ALLM compound as proteasome; OTHER INFORMATION: inhibitor US-09-695-807-2
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Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                     Query Match 52.0%; Score 13; DB 5; Length 4; Best Local Similarity 100.0%; Pred. No. 6.2e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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US-09-931-009A-2	25	1 GPRP 4
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86

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65 summaries

Database :

PIR 78:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query	;	}	SUMMAKIES	
,	Score	Match	Length	B	ID	Description
	13	52.0	4	0	PT0675	T-cell receptor be
	12	48.0	4	7	A02147	phagocytosis-stimu
	7	28.0	٣	m	RHTDTO	thyroliberin - Bom
	7	28.0	٣	m	RHPGT	1
	7	œ	m	m	RHSHT	thyroliberin - she
	7	28.0	m	ო	A92971	1
	7	28.0	m	m	A33802	Q
	7	8	m	m	A43391	TRH-like tripeptid
	7	28.0	٣	m	I78890	tyrosine protein k
	7	æ	4	7	A32039	tyrosine-melanocyt
	7	28.0	4	~	PL0140	carbon-monoxide de
	7	æ	4	7	\$53508	starvation-induced
	7	8	4	0	S17255	ribosomal protein
	7	8	4	7	A34626	RPCH-related neuro
	7	28.0	4	~1	I51049	metallothionein-A
	7	28.0	4	Ŋ	PT0240	Ig heavy chain CRD
	7	28.0	4	N	154357	schwannomin - mous
	Q	4.	m	'n	GKHU	growth-modulating
	9	24.0	m	ო	A60898	bursin - chicken
	9	4.	m	ო	A23751	
	Q	4	m -	m	B23751	cord
	9	4.	m	m	PT0636	recei
	9	4	m	m	PT0571	
	9	4	4,	Н	ECXAA	antho-RFamide neur
	9	24.0	4	(1	T30569	hypothetical prote
	9	24.0	4	8	138888	w
	9	4.	4	7	A25844	amide
	9	24.0	4	N	ω	achatin-I - giant
	9	24.0	4	N	839390	myosin-light-chain

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000000	2 PT069 2 PT070 2 PT070 2 PT072 2 S4755	2 A2256 3 A2256 3 A2256 2 ECNK 2 D4165 2 I4087	01 01 01 01 01 01 01 01 01 01 01 01 01 0	4 2 140005 4 2 140004 4 2 746627 4 2 701273 4 2 844823 4 2 PT0534 4 2 A48050 4 2 157745 3 3 150412
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ALIGNMENTS

PESULI 1 PRESULI 1 PRESULI 1 PRESULI 1 PROFOST T-cell receptor beta chain V-D-J region (140-1AC) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 17-Jul-1992 #text_change 30-May-1997 C;Accession: PT0675 R;Feeney, A.J. J. Exp. Med. 174, 115-124, 1991 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:171558 A;Accession: PT0675 A;Accession: PT0675 A;Accession: PT0675 A;Accession: PT0675 A;Accession: PT0675 A;Accession: T0675 A;Residues: 1-4 <fee> A;Residues: 1-4 <fee> A;Residues: 1-4 <fee> A;Experimental source: day 18 fetal thymus, strain BALB/C C;Keywords: T-cell receptor C;Keywords: T-cell receptor C;Keywords: T-cell sequences of Mismatches D; Indels 0; Gaps 0; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</fee></fee></fee>
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RESULT 2
A02147
plagocytosis-stimulating peptide (tuftsin) - human
pragocytosis Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Feb-1994
C;Accession: A02147

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 4

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Query Match
Best Local Similarity
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Rivishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
Biochem. Biophys. Res. Commun. 47, 172-179, 1972
A;Title: The characteristics, isolation and synthesis of the phagocytosis stimulating pe A;Reference number: A02147; MUID:72187087; PMID:4112769
A;Accession: A02147
A;Accessi
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RyNair, R.W.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.
A; Harry 9, 1103-1106, 1970
A; Title: Structure of porcine thyrotropin releasing hormone.
A; Reference number: A90560; MUID:70136150; PMID:4984938
A; Accession: A01415
A; Molecule type: protein
A; Residues: 1-3 < MAI>
A; Molecule type: protein
A; Residues: 1-3 < MAI>
A; Roller, J; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.
B; Blochen. Biophys. Res. Commun. 37, 705-710, 1969
A; Title: The identity of chemical and hormonal properties of the thyrotropin releasing B; Reference number: A00167; MUID:70039904; PMID:4982117
A; Reference number: A00167; MUID:70039904; PMID:4982117
A; Roter annotation
A; Rote: biological activities and Rf values (in 17 chromatographic systems) of the syntle: Superfamily: thyroliberin precursor
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C;Date: 15-Unn-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A90919; A01415
R;Yasuhara, T.; Nakajima, T.
Chem. Pharm. Bull: 33, 3301-3303, 1975
A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
A;Reference number: A90919; MUID:76138399; PMID:815011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thyroliberin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A01415
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C, Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
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A,Molecule type: protein
A,Molecule type: protein
A,Residues: 1-3 <7AS>
C,Superfamily: thyroliberin precursor
C,Superfamily: thyroliberin precursor
C,Keywords: amidated carboxyl end, cutaneous gland, hormone, pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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stidine, or glutamic acid
C;Superfamily: thyroliberin precursor
C;Superfamily: thyroliberin precursor
C;Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic & F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Ovis orientalis aries, Cvis ammon aries (domestic sheep)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A93750; A0415
R;Desiderio Jr, D., D., Burgs, R; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimulating
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C, Superfamily: thyroliberin precursor
C, Superfamily: thyroliberin precursor
C, Styeywords: amidated carboxyl and; hormone; hypothalamus; pyroglutamic acid
F, 1/Modified site: pyrrolidone carboxylic acid (Gin) #status experimental
F, 3/Modified site: amidated carboxyl end (Pro) #status experimental
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A,Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brai A,Reference number: A92971; MUID:75035605; PMID:4214528
A,Accession: A92971
A,Molecule type: protein
A,Residues: 1-3 cGRI>
A,Note: a peptide with the chromatographic and electrophoretic characteristics of thyroli
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A;Accession: A93750
A;Accession: A93750
A;Accession: A93750
A;Accession: A93750
A;Residues: 1-3 < DES>
B;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
Nature 226, 321-325, 1970
A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor. A;Reference number: A93161; MUID:70163386; PMID:4988794
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
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llarity 100.0%; Pred. No. 2.8e+05;
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                                                                                                               A Score 7; DB 3; Le Similarity 100.0%; Pred. No. 2.8e+05; 1; Conservative 0; Mismatches 0;
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tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A32039
R;Horvath, A.; Kastin, A.;
J Biol. (Chem. 264, 2175-2179, 1989
A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1
A;Reference number: A32039; MUID:89123285; PMID:2563371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carbon-monoxide dehydrogenase (BC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena C;Species: Pseudomonas carboxydohydrogena C;Species: Pseudomonas carboxydohydrogena C;Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993 C;Accession: PL0140 C;Accession: PL0140 B;Xxaut, M.; Hugendieck, I.; Herwig, S.; Meyer, O. Arch. Microbiol. 152, 335-341, 1989 A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotroph A;Reference number: PL0138; MUID:90055678; PMID:2818128 A;Accession: PL0140 A;Accession: PL0140 A;Accession: PL0140 A;Accession: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, mec C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, mec C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              starvation-induced ribonuclease - tomato
Cispecies: Lycopersicon esculentum (tomato)
Cipacies: Lycopersicon esculentum (tomato)
Cipacession: 853508
Kivoeck, M.; Loeffler, A.; Abel, S.; Glund, K.
Plant Mol. Biol. 27, 477-485, 1995
A;Title: cDNA structure and regulatory properties of a family of starvation-induced ribor
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A,Rolecule type: protein
A,Rolecule type: protein
A,Residues: 1-4 - 40Rx - A.Experimental source: brain
C,Superfamily: unassigned animal peptides
C,Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental
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Query Match 28.0%; Score 7; DB 3; Length 3; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 1; Conservative 0; Mismatches 0; Indels
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A; Status: preliminary
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S53508
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PL0140
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tyrosow musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Joace: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C.Joacession: 178890

R.Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.

Oncogene 9, 3437-3448, 1994

A.Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine proteil

A.Accession: 178890

A.Accession: 178890

A.Accession: 178890

A.Fathus: preliminary; translated from GB/EMBL/DDBJ

A.Residues: 1-3 <RES>

A.Residues: 1-3 <RES>

A.Gross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538
                                                                                                                                                                                                              C)Accession: A33802 A.; Beg, F.; Smyth, D.G.
J. Scotle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.
J. Biol. Chem. 264, 7788-7791, 1989
A;Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate comp.
A;Reference number: A33802; MUD:89255196; PMID:2498305
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRH-11ke tripeptide - alfalfa
C:Species: Medicago sativa (alfalfa)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A43391
R:Lackey, D.B.
A:D Biol. Chem. 267, 17508-17511, 1992
A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-A;Reference number: A43391; MUID:92388092; PMID:1517203
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                                                                                                                                                         C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-3 <COC>
(S.Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
E;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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A;Residues: 1-3 <LAC>
C;Keywords: amidated carboxyl end, pyroglutamic acid
F;1/Wodified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Wodified site: amidated carboxyl end (Pro) #status experimental
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                                                                                                                         thyrotropin-releasing hormone-like peptide - rabbit
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A, Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) met A, Reference number: 151049; MVID:95324545; PMID:7601121
A, Accession: 151049
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-4 < OLS>
A, Residues: 1-4 < OLS>
A, Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: Pr0240
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc.
A;Reference number: PT0222; MUID:91108337; PMID:1899102
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R.Huynh, D.P.; Nechiporuk, T.; Pulst, S.
R.Hui, No. Genet. 3, 1075-1079, 1994
A; Reference number: 154357; MUID:95072570; PMID:7981675
A; Accession: 154357
A; Accession: 154357
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-4 <RES>
A; Residues: 1-4 <RES>
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            schwannomin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
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28.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels
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C;Species: Homo sapiens (man)
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Best Local Similarity
Matches 1; Conserv
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A; Residues: 1-4 < YAM>
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A;Title. Amolluscan neuropeptide related to the crustacean hormone, RPCH.
A;Reference number: A34626; MUID:90179762; PMID:2310394
A;Reference number: A34626
A;Resion: A34626
A;Resion: A34626
C;Reywords: neuropeptide
C;Reywords: neuropeptide
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A,Residues: 1-4 <GRO>
C,Comment: A coding region for this protein could not be identified in the genome of Sad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rigrohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M. FEBS Lett. 284, 51-56, 1991
A-Titlels Extended N-terminal sequencing of proteins of the large ribosomal subunit from A; Reference number: S17255; MUID:91285106; PMID:2060626
                                                                                                                                                                                                                                                                                                                                                                                                                            ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)
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A/aariev. strain 07173
C.Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
C.Accession: S17255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Species: Fusinus ferrugineus (ferruginous spindle)
C,Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
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28.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels
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C;Keywords: mitochondrion; protein biosynthesis; ribosome
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      A, Molecule type: protein A, Residues: 1-4 < KOE>
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spinal cord peptide SCP-5 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: B23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, A.K.cession: B23751
A;Reference number: A23751; MUID:85250425; FMID:4015098
A;Accession: B23751
A;Accession: preliminary
A;Acture preliminary
A;Acture preliminary
A;Molecule type: protein
A;Residues: 13 <HSI>
C;Superfamily: unassigned animal peptides
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J. Exp. Med. 174, 115-124, 1991
J. Exp. Med. 174, 115-124, 1991
A.Jitlei Juncational sequences of fetal T cell receptor beta chains have few N regions.
A.Reference number: PT0509; MUID:91277601; PMID:1711558
A.Accession: PT0636
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C;Species: Mus musculus (house mouse)
C;Species: IS-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PTG571
R;Feeney, A.J.
T, 115-124, 1991
A;Tible: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0636
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24.0%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels
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24.0%; Score 6; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
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A;Molecule type: mRNA
A;Residues: 1-3 cFEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
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A;Status: translation not shown
A;Molecule type: mRNA
A;Experiments: 13 orEES
C;Keywords: T-cell receptor
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: A60898
R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 211, 997-999, 1986
A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of A;Teference number: A60898; MUID:86122916; PMID:3464838
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A23751
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, Arch. Blochem. Blophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425; PMID:4015098
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     15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
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                              CyAccession: A01421
Ryschlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 344-325, 1977
A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A;Reference number: A01421; MUID:77162369; PMID:858356
A;Accession: A01421
A;Molecule type: protein
A;Note: 13 accMa
A;Note: this serum tripeptide is found to stimulate growth of some celc;Superfamily: unassigned animal peptides
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A,Residues: 1-3 <AUD>
C,Superfamily: unassigned animal peptides
C,Keywords: amidated carboxyl end; hormone
F,3/Modified site: amidated carboxyl end (Gly) #status experimental
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-3 <HSI>
C,Superfamily: unassigned animal peptides
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RjGrimmelikhuijzen, C.J.P.; Groeger, A.
Fabs Lett. 211, 105-108, 1987
A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renills.
A;Reference number: A25844
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R;Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun, Blochem. Blophys. Res. Commun. 160, 1015-1020, 1989
A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica ferus A;Reference number: A32480; WUID:89273551; PMID:2597281
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A,Residues: 1-4 <KAM>
A,Note: stereochemistry of the active form confirmed by chemical synthesis
B,Note: T: In, Y: Inoue, M: Yasuda-Kamatani, Y: Minakata, H:; Iwashita, T.; Nomoto, FBBS Lett. 307, 253-256, 1992
A,Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neurog
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C;Species: Renilla koellikeri (Koelliker's sea pansy)
C;Date: 21-May-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997
C;Accession: A25844
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C;Species: Achatina fulica (giant African snail)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
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A;Contents: annotation; X-ray crystallography, 0.85 angstroms
A;Note: acchain-II has L-phenylalanine
C;Reywords: D-amino acid
F;2/Modified site: D-phenylalanine (Phe) #status experimental
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Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels
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C; Keywords: mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T30569
R;Morrice, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
Curr. Genet. 34, 379-385, 1998
A;Title: Isolation and characterisation of the acetyl-CoA carboxylase gene from Aspergil
A;Reference number: 220869; MUID:99087906; PMID:9871120
                                                                                       antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)
()Species: Anthopleura elegantissima
()Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
()Accession: A26666
R;Grimmelikhuijzen, C.J.P.; Graff, D.
R;Grimmelikhuijzen, C.J.P.; Graff, D.
A;Title: Isolation of sglu-gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anem A;Reference number: A26666; MUID:87092339; PMID:2879288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: mitochondrion Podospora anserina
C;Date: 03-Peb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999
C;Accession: 138888
R;Cummings, D.J.; Michel, F; McNally, K.L.
Curr. Genet. 16, 381-406, 1989
A;Title: DAA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I mi
A;Reference number: A48327; MUID:90124722; PMID:2558809
                                                                                                                                                                                                                                                                                                                                                                  A,Accession: A2666
A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
C,Comment: The function of this peptide is not known but it could act as a transmitter C,Comment: Synthetic and natural peptides had identical properties.
C,Superfamily: RFamide neuropeptide
C,Keywords: amidated carboxyl end, neuropeptide, pyroglutamic acid
F,I/Modified site: pyrrolidone carboxylic acid (Gin) #status experimental
F,I/Modified site: amidated carboxyl end (Phe) #status experimental
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A,Scatus: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Rosidues: 1-4 < MOR>
A;Cross-references: EMBL:Y15996; NID:e1285512; PID:e1218041; PIDN:CAA75927.1
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24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels
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A,Cross-references: GB:X55026; GB:M30937; GB:M61734
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A; Genome: mitochondrion A; Genetic code: SGC3

A;Status: preliminary A;Molecule type: DNA A; Accession: 138888 A; Status: prelimina

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RESULT 26

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Query Match Best Local Similarity Matches 1; Conserv

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RESULT 25

0; Indels

Length 4;

Query Match
24.0%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0;

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T-cell receptor beta 2 chain D region, Dbeta2 - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C;Accession: A53284 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 R;Harindranath, N ; Alexander, C.B.; Mage, R.G. Mol. Immunol. 28, 881-888, 1991 A;Title: Evolutionarily conserved organization and sequences of germline diversity and jc A;Reference number: A53284; MUID:91342695; PMID:1678859
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Dacte: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B51284 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline div A;Reference number: A53284; MUID:91342695; PMID:1678859
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19517.1; PID:g233917
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60739)
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-4 <HAR>
A,Cross-references: GB.S60737; NID:g233916; PIDN:AAB19518.1; PID:g233918
A,Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C,Keywords: T-cell receptor
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Similarity 100.0%; Pred. No. 2.8e+05;
1; Conservative 0; Mismatches 0;
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C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
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Best I Conservative
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Best Local Similarity
Matches 1; Conserv
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A;Molecule type: DNA
A;Residues: 1-4 <HAR>
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R; Feeney, A.J.
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myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - turkey (fragment)
C;Species: Meleagris gallopavo (common turkey)
C;Accession: S39390
C;Accession: S39390
E;Komateu, H.; Tkebe, M.
Biochem J. 296, 53-58, 193
A;Title: Affinity labelling of smooth-muscle myosin light-chain kinase with 5'-[p-(fluor Affinity labelling of smooth-muscle myosin light-chain kinase with S'-[p-(fluor Affinity labelling of smooth-muscle myosin light-chain kinase with S'-[p-(fluor Affinity labelling of smooth-muscle myosin light-chain kinase with S'-[p-(fluor Affinity labelling of smooth-muscle myosin light-chain kinase with S'-[p-(fluor Affinity labelling of smooth-muscle myosin light-chain kinase with S'-[p-(fluor Affinity labelling of smooth-muscle myosin light-chain kinase with S'-[p-(fluor Affinity labelling of smooth-muscle kikeywords: labelling of smooth muscle
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0271.
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0221; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S43959
Ig mu chain V region (clone 13) - human (fragment)
Ig mu chain V region (clone 13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S43959 #sequence_revision, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, Iskyagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, Iskurieic Acids Res. 22, 1389-1393, 1994
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
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h Similarity 100.0%; Pred. No. 2.8e+05; 1; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity

Matches

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RESULT 31

A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

24.0%; Score 6; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 1, Conserv

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RESULT 32

A,Molecule type: DNA A,Residues: 1-4 <WAG> C,Keywords: immunoglobulin

A; Accession: S43959

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Gaps

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Indels

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J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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A;Title: Unactional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R;Feeney, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell receptor beta chain V-D-J region (126-1BG) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Bate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 C;Accession: PT0558; PT0677 R;Feeney, A.J.
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 14 <FE3.
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2C
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: PT0558
A,Status: translation not shown
A,Molecule type: mRNA
A,Residues: 1-4 <PEE>
A,Experimental source: day 18 fetal thymus, strain BALB/c, 126-1BG
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A;Molecule type: DNA
A;Residues: 1-4 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1BH
C;Keywords: T-cell receptor
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                                                                                                                                                                         Query Match
24.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels
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A;Residues: 1-4 <FRES
A;Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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Best Local Similarity
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A/Title: Junctitional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0607
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Dete: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Sep-1997
C;Accession: PT0546; PT0698; PT0583
                                                                                                                                                                                                                                                                                                        Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997; Accession: PT0607; PT0674; PT0678; PT0570; PT0111; PT0710
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                                                                                                                                                                                                                                                receptor beta chain V-D-J region (120-2J) - mouse (fragment)
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Experimental source: newborn thymus, strain BALB/c, 120-2J
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A;Molecule type: mRNA
A;Residues: 1-4 <FE4>
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A;Molecule type: DNA
A;Residues: 1-4 <FE5>
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A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
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Molecule type: DNA
Residues: 1-4 <FE2>
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Status: translation not shown
Molecule type: DNA
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Globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
NyAlternate names: 11S globulin alpha subunit gamma chain
C;Species: Cucurbita sp. (cucurbit)
C;Species: Cucurbita sp. (cucurbit)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
C;Accession: S09478
R;Ohmiya, M.; Hara, I. Matsubara, H.
Plant Cell Physiol. 21, 157-167, 1980
A;Thile: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and PA;Reference number: S09066
A;Accession: S09478
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Agric. Biol. Chem. 3, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiotensin-converting enzyme inhibitor (FLP-3) - common fig
N;Alternate names: ficus latex peptide 3
C;Species: Ficus carica (common fig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PQ0010
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20.0%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indel.
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A,Molecule type: protein
A,Residues: 1-3 <MAR>
A,Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor
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Best Local Similarity
Matches 1; Conservat
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
Cisconin 547552
Ribubard, M.J.; Carne, A.
Bicchin Biophys. Acta 1200, 191-196, 1994
A;Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat
A;Reference number: 847552
A;Accession: 847552
A;Accession: 847552
A;Accession: A;Accession:
                    C. Species: Mus musculus (nouse mouse)
C. Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C. Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C. Accession: PT0721
B. FED. Med. 174, 115-124, 1991
A. FILLE: Unactional sequences of fetal T cell receptor beta chains have few N regions.
A. Reference number: PT0721
A. Accession: PT0721
A. Accession: PT0721
A. Accession: PT0721
A. Molecule type: DNA
A. Residues: 1-4 < FEE>
A. Experimental source: newborn thymus, strain BALB/C
C. Keywords: T-cell receptor
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A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Recession: PT056
A/Recassion: PT056
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A/Recassion: A/Recassion: PT056
A/Recassion: Land A/Recassion not shown
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PT0566
Coll receptor beta chain V-D-J region (141-1CH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0566
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receptor beta chain V-D-J region (140-2K) - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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protamine PI - orangutan (fragment)
C;Species: Pongo pygmaeus (orangutan)
C;Species: Pongo pygmaeus (orangutan)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C;Accession: 161883
R;Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A;Title: 197-204, 1993
A;Reference number: 137013; MUID:94040810; PMID:8224908
A;Accession: 161883
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Anthopleura elegantissima
C.Species: Anthopleura elegantissima
C.Species: Anthopleura elegantissima
C.Species: A-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 08-Dec-1995
C.Accession: A3579
R.Grimmellikhuijzen, C.J.P.; Rinehart, K.L.; Jacob, E.; Graff, D.; Reinscheid, R.K.; Nothe R.Grimmellikhuijzen, C.J.P.; Rinehart, K.L.; Jacob, E.; Graff, D.; Reinscheid, R.K.; Nothe A; Grimmellikhuijzen, C.J.P.; Rinehart, L.J. Jacob, E.; Graff, D.; Reinscheid, R.K.; Nothe A; Title: Isolation of E.J. Phenyllactyl-Leu-Azg-Asn-NH2 (Antho-RNamide), a sea anemone net A; Reference number: A35779; MUID:90319122; PMID:1973541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an amino-terminal phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Nereis virens (sandworm)
C.Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 11-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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R;Krajniak, K.G.; Price, D.A.
Peptides 11, 75-77, 1987
A;Title: Authentic FMRFamide is present in the polychaete Nereis virens.
A;Reference number: A60418; MUID:90259866; PMID:2342992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A35779
A;Rolecule type: protein
A;Residues: 1-4 <GRI>C;Comment: The L-3-phenyllactyl blocking group probably arises from C;Comment: The L-3-phenyllactyl end; neuropeptide; phenyllactylation C;Keywords: amidated carboxyl end; neuropeptide; phenyllactylation F;I/Modified site: L-3-phenyllactic acid (Phe) #status experimental F;4/Modified site: amidated carboxyl end (Asn) #status experimental
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Similarity 100.0%; Pred. No. 2.8e+05;
1; Conservative 0; Mismatches 0; Indele
                      DB 2; Length . 2.8e+05;
       20.0%; Scor.
100.0%; Pred. No. ...
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A;Title: Tole of the upstream region containing an intrinsic DNA curvature in the negation A;Reference number: 140870; MUID:92396045; PMID:1522810
A;Accession: 140870
                                                                                                                                                                                                                                                    C)Accession: A0126
R:Price, D.A.; Greenberg, M.J.
Science 197, 670-671, 1977
A;Title: Structure of a molluscan cardioexcitatory neuropeptide.
A;Reference number: A01426; MUD:77215956; PMID:877582
A;Reference number: A01426
A;Reference number: A01426
A;Reference number: A01426
A;Residues: 1-4 < PRI>
A;Residues: 1-4 < PRI
A;Residues
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C'Species: Haemophilus parainfluenzae
C'Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phospholipase C (EC 3.1.4.3) - Clostridium perfringens (fragment)
C;Species: Clostridium perfringens
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000
C;Accession: I40870
                                                                                                                                                                                        C;Species: Macrocallista nimbosa (sunray clam)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X62825; NID:g40622; PIDN:CAA44636.1; PID:g4377417
C;Genetics:
A;Gene: plc
C;Xeywords: phosphoric diester hydrolase
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                                                                                                                                                  - sunray clam
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A;Molecule type: DNA
A;Residues: 1-4 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.0%; Score 5; DB 2 Best Local Similarity 100.0%; Pred. No. 2.8 Matches 1; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 2.8
Matches 1; Conservative 0; Mismatches
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A;Molecule type: DNA
A;Residues: 1-4 <KRO>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <RES>
A;Cross-references: EMBL:Z12146; NID:g38156; PIDN:CAA78130.1; PID:g4379372
```

Query Match

20.0%; Scree 5, DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2,8e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: September 7, 2004, 19:25:39 Job time : 16 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 7, 2004, 19:21:52; Search time 9 Seconds (without alignments) 23.142 Million cell updates/sec Run on:

US-09-931-009A-2 25 1 GPRP 4 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

18 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 4

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

otion	homo sapien	sus scrofa	pseudomonas	saccharomyc	homo sapien	achatina fu	homo sapien	octopus min	octobus min	hirudo medi	hirudo medi	hirudo medi	anthopleura	macrocallis	anthopleura	vibrio fisc	pseudomonas	anthopleura
Description	P01858	P01151	P19916	P36515	P01157	P35904	P02731	P58648	P58649	P42562	P42563	P42561	P58707	P01162	P58706	P24272	P19918	P58705
	TUFT HUMAN	HYL_PIG	PSECH	RM01 YEAST	GRWM HUMAN	ACHFU	HUMAN	OCTMI	OCTMI	HIRME	FAR4 HIRME	_HIRME	ANTEL	MACNI	ANTEL	VIBFI	DCMS_PSECH	ANTEL
OI .	TUFT	THYL	DCML	RMO1	GRWM	ACH1	EOSI	OCP1	OCP3	FAR3	FAR4	FLRF	FLRN	FMRF	FYRI	LUXE	DCMS	FFKA
DB	Н	Н	Н	Н	Н	Н	Н	Н	H	Н	Н	Н	H	Н	Н	Н	Н	Н
% Query Match Length DB	4	т	4	4	m	4	4	4	4,	4	4	4	4	4	4	m	4	4
% Query Match	48.0	28.0	28.0	28.0	24.0	24.0	24.0	24.0	24.0	20.0	20.0	20.0	20.0	20.0	20.0	8.0	9.0	8.0
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Result No.	-	(7)	m	4	w	Φ	7	œ	თ	10	11	12	13	14	15	16	17	18

ALIGNMENTS

							Euteleostomi;
	4 AA.		update)	n_update)	ftsin),		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	; PRT;	21-JUL-1986 (Rel. 01, Created)	ast sequence u	ast annotation	Phagocytosis-stimulating peptide (Tuftsin),		rdata; Craniat
	STANDARD;	5 (Rel. 01, C1	6 (Rel. 01, La	. (Rel. 40, La	s-stimulating	s (Human).	Metazoa; Chor
RESULT 1 TUFT HUMAN	TUFT HUMAN P01858;	21-JUL-1986	21-JUL-1986	16-0CT-2001	Phagocytosi	Homo sapiens (Human).	Eukaryota;
RESI	AC AC	DŢ	DŢ	DΤ	DE	SO	00

Mammalia, Butheria, Primates; Catarthin; Hominidae; Homo. MAMMalia, Butheria, Primates; Catarthin; Hominidae; Homo. MCGL_TAXID=5666; MCGL_TAXID=5666; MCGL_TAXID=5666; MCGL_TAXID=5666; MCGL_TAXID=5666; MILIALING PROPER, ISOSIATION A. Sarch P. S., Najjar V. N.; MCGL_MCGL_MCGL_MCGL_MCGL_MCGL_MCGL_MCGL_
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SEQUENCE

SEQUENCE

RRITER REPRESENTATION OF SECOND SECON

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-!- COFACTOR: Molybdenum (molybdopterin).
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
MEDLINE=91285106, PubMed=2060626;
Grobmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
Kitakawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-77162369; PubMed-858356;
Schlesinger D.H., Pickart L., Thaler M.M.;
Schlesinger B.H., Pickart L., Thaler M.M.;
"Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
Experientia 33:324-325 (1977).
-!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
growth of some cell types and to inhibit other types in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; PERS Lett. 284:51-56(1991). PERS 17255; S17255; S17255 SQP; LO002681; MRPL1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Mitochondrial 60S riboscmal protein L1 (YmL1) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.0%; Score 7; DB 1; Length 4; llarity 100.0%; Pred. No. 1.4e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   DB 1; Length 4; . 1.4e+05;
                                                                                            PIR; PLO140; PL0140.
Oxidoreductase; Molybdenum.
NON TER 4 4
SEQÜENCE 4 AA; 441 MW; 7761E876F000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AA; 402 MW; 7771B2D5D000000 CRC64;
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ALD GRWM HUMAN STANDARD; PRT; 3 AA.
ALD 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AA.
                                                                                                                                                                                                                                               11arity 100.0%; Score 7; DB 1 101arity 100.0%; Pred. No. 1.4 Conservative 0; Mismatches
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Best Local Similarity
Matches 1; Conservat
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les 1, Conserv
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C4 --
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SEQUENCE
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RM01_YEAST
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Matches
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-1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/ neuromodulator in the central and peripheral nervous systems.
      stimulating hormone releasing factor of ovine origin by means of mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=N viridescens;
MEDLINE=75035605, PubMed=4214528;
Grimm-Joergensen Y., McKelvy J.F.;
Blosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
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01-FEB-1991 (Rel. 17, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=B.orientalis; TISSUE=Skin;
MEDLINE=76138399; PubMed=815011;
Yasuhara T., Nakajima T.;
"Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
Chem. Pharm. Bull. 23:3301-3303(1975).
                                                                                                                                                                 SPECIES-Sheep;
MEDILIBE-70163386; PubMed-4985794;
BUTGUS R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
Guillemin R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amidation; Pyrrolidone carboxylic acid.
MOD_RES 1 PRENOLIDONE CARBOXYLIC ACID.
MOD_RES 3 AMIDATION.
SEQUENCE 3 AA, 380 MW, 7761F6B00000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                       "Characterization of ovine hypothalamic hypophysiotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.0%; Score 7; DB 1; Length 3; llarity 100.0%; Pred. No. 1.4e+05; Conservative 0; Mismatches 0; Indele
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                                          spectrometry.";
Org. Mass Spectrom. 5:221-228(1971).
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                                                                                                                                                                                                                                                                                                                    TSH-releasing factor.";
Nature 226:321-325(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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PIR; A92971; A92971.
PIR; A93750; RHSHT.
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P19916;
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Query Match

Best Loc Matches

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DCML_PSECH

RESULT 3

SEQUENCE

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Gaps

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RESULT 6 ACH1_ACHFU

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Analogy axis.

Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

(and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting ecosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.

GO, GO:0006935; P:chemotaxis; IDA.

GO; GO:0006955; P:immune response; IDA.

V -> A (IN OTHER PEPTIDE).

/ FTId=VAR 005201.

SEQUENCE 4 AA; 390 MW; 6B05B862A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=76078412; PubMed=1060093; Goetzl B.J., Austen K.F.; Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20336815; PubMed=10876044;
Iwakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
Peptides 21:623-630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazos; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea; Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
NCBL_TaxID=89766;
                                                                                                                                                                                                       Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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FUNCTION: Cardioactive; has both positive chronotropic an inotropic effects on the heart. Ocp-2 is a 1000 time less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
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        MOD RES
        2
        D-PHENYLALANINE (IN OCP-1)

        SEQUENCE
        4 AA; 394 MW; 6AA879C810000000 CRC64;

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-- SUBCELLULAR LOCATION: Secreted.
--- PTM: OCp-2 has L-Phe instead of D-Phe.
--- MASS SPECTROMETRY: WW=395.2; METHOD=MALDI.
                                                                       Last sequence update)
Last annotation update)
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PFBB-2003 (Rel. 41, Last sequenc,
15-MAR-2004 (Rel. 43, Last amotat.
Cardioactive peptides Ocp-1/Ocp-2.
                                          Created)
                                   21-JUL-1986 (Rel. 01, Creat
21-JUL-1986 (Rel. 01, Last
21-JUL-1986 (Rel. 01, Last
Eosinophilotactic peptides.
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                                                                                                                                                                           Homo sapiens (Human)
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Best Local Similarity
Matches 1; Conserv
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OCP1_OCTMI
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          STANDAR REPARENCE OCCOUNTY OF THE PROPERTY OF 
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Int. J. Pept. Protein Res. 39:258-264 (1992).

Int. J. Pept. Protein Res. 39:258-264 (1992).

Int. J. Pept. Structure Res. 39:258-264 (1992).

Int. J. Pept. Protein Res. 39:258-264 (1992).

Int. J. Pept. Structure Res. 39:258-264 (1992).

PURJAGON; Also enhances the amplitude and frequency of the heart beat. Has also an effect on several other muscles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Achatina fulica (Giant African snail).
Bukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata; Stylommatophora,
Bigmurethra, Achatinoidea, Achatinidae, Achatina.
NCBI_TaxID=6530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Ferussac; TISSUE=Ganglion; MEDLINE=8227351; PubMed=2597281; Ramatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Funase K., Sun X.P., Yongairi A., Kim K.H., Nowales-Li P., Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.; An endogenous neuroexcitatory tetrapeptide from Achatina fulica Ferussac containing a D-amino acid residue."; Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Ferussac; TISSUE=Heart atrium; MEDINE=91264856; PubMed=1675568; Pulinnoto X., Kuboca I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.; Putrification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function."; Biochem. Biophys. Res. Commun. 177:847-853(1991).
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                                                                                                24.0%; Score 6; DB 1; Length 3; 100.0%; Pred. No. 1.4e+05; 1ve 0; Mismatches 0; Indels
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GO; GO: 0001558; P: regulation of cell growth; NAS. SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;
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4 AA; 408 MW; 6AADD9C810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                                                                                Similarity 100.0%;
1; Conservative 0
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Best Local Similarity
Matches 1; Conserv
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ID _EOSI_HUMAN
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TISSUB-Brain;
MEDLINE-20336815; PubMed=10876044;
IWakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
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                                                                                                       Octopus minor (Octopus).
Bukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Octopodiformes, Octopoda, Incirrata, Octopodidae, Octopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE=92195954; PubMed=1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Lidentification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-: SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
FURL and a mideration update)
FMRFamide-11ke neuropeptide YLRF-amide
Hirudo medicinalis (Medicinal leech).
Bukaryora, Merazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudinea;
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MOD RES 4 4 AMIDATION.
SEQUENCE 4 AA; 598 MW; 69D4073B3000000 CRC64;
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4 AA; 463 MW; 6AB365B810000000 CRC64;
                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cardioactive peptides Ocp-3/Ocp-4.
                          4 AA.
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Best Local Similarity
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Matches 1; Conserv
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ID FAR3 HIR
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RESULT 9
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Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.; "FWRFamide-related peptides from the kidney of the snail, Helisoma
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                                                                                                                                                                           MEDIINE=22195954; PubMed=1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-:- SIMILARITY: Belongs to the FARP (FWRFamide related peptide)
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=H.medicinalis;
MEDLINE=22195954; PubMed=1686933;
Varus B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of Remaide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIRFamide.
Firston medicinalis (Medicinal leech), and
Helisoma trivolis (Snail).
Eukaryota, Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudinida.
                                                        01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide YMRF-amide.
Hirudo medicinalls (Medicinal lecch).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudio.
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-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                            (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
4 AA.
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PRT;
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Best Local Similarity 100..
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MOD RES 4 4
SEQUENCE 4 AA; 616 MW;
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                              01-NOV-1995
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 FAR4 HIRME
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100.0%; Pred. No. 1.4
1tive 0; Mismatches
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                                        SPECIES=N.virens;
MEDLINE=90259866; PubMed=2342992;
Prep. Biochem. 7:261-281(1977)
                                                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide, Amidation.
MOD_RES 4 4
SEQUENCE 4 AA; 600 MW;
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PIR; A60418; A60418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Price D.A., Greenberg M.J.; "Purification of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Sukaryota; Metazoa; Mollusa; Heteroconchia; Veneroida;
Veneroidea; Veneridae; Macrocallista.
NCBI_TaxID=6594, 6353, 6421, 27815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=M.nimbosa, TISSUE=Cerebral pedal, and Visceral ganglion, MEDLINE=77215956; PubMed=877592, Price D.A., Greenberg M.J.; Structure of a molluncan cardioexcitatory neuropeptide."; Science 197:670-671(1977).
                                                                                                                                                                         Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
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21-JUJ-1986 (Rel. 01, Last sequence update)
15-JUJ-1998 (Rel. 36, Last annotation update)
MRFPamide (Peak C) (Cardioexcitatory neuropeptide)
Macrocallista nimbosa (Sun-ray clam),
Nereis virens (Sandworm),
Hirudo medicinalis (Medicinal leech), and
                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AMIDATION.
549 MW; 64540729A0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990)
-!- SUBCELDULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
-!- TISSUE SPECIFICITY: MW=549.3; METHOD=FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                     L-3-PHENYLLACTYL
                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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SEQUENCE, AND CHARACTERIZATION.
SPECISS=M.nimbosa, TISSUE=Ganglion;
MEDLINE=78012038, PubMed=909875;
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                                                                                                                                                                                                                                               SEQUENCE, AND MASS SPECTROMETRY.
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MOD_RES 1 1
MOD_RES 4 4
SEQUENCE 4 AA; 549 MW.
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nes 1; Conserv
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                                                                                                                                                                                                                                                                                                                               group."
                                                                 RESULT 13
FLRN ANTEL
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Matches
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Peptides 15:31-36(1994).
-!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
activities include augmentation, induction, and regularization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-H.trivolvis; TISSUE-Kidney;
MEDINE-9428417; PubMed-79128;
Madrid K.P., Price D.A., Zreenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation of two novel neuropeptides from sea anemones: the unusual, biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-phenyllactyl fragment Tyr-Arg-Ile-NH2."; Peptides 12:1165-1173(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93391436; PubMed=8397415; MCFATINE 1.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.; MCFATIANE 1.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.; The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Khamide and Antho-Riamide."; Proc. R. Soc. Lond., B. Biol. Sci. 253:188-188193).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding
                                                                                                                                                                                SPECIES-H.medicinalis;
MEDLINE-92195954; PubMed-1686933;
MEDLINE-92195954; PubMed-1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
Krajniak K.G., Price D.A., "Authentic FMRFamide is present in the polychaete Nereis virens."; Peptides 11:75-77(1990),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI TaxID=6110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac contraction.
-!- SIMILARITY: Belongs to the PARP (FWRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . DB 1; Le...
No. 1.4e+05;
O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE=92270459; PubMed=1821096;
Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
Grimmelikhuijzen C.J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AA; 600 MW; 69D40699A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
88-FEB-2003 (Rel. 41, Last annotation update)
Antho-Rlamide I [Contains: Antho-Rlamide II].
Anthopleura elegantissima (Sea anemone)
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acceptor.
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P58705;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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         SO THE STATE OF THE SO 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SILE for the lux operon.;

J. Bacteriol. 172:6797-6802 (1990).

- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.

- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.

IT IS A COMPONENT OF THE PATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.

- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.

- PATHWAY: Bioluminescent fatty acid reduction system; second step.
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=91072226; PubMed=2254256;
Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                              DB 1; Length 4;
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                                                                                                                    1 4 ANTHO-RIAMIDE I.

2 4 ANTHO-RIAMIDE II.

1 1 L-3-PHENYLLACTYL.

4 AMIDATION.

4 AA; 598 MW; 60441B59A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER 1 1 1 1 SEQUENCE 3 AA; 374 MW; 6AA330300000000 CRC64;
                                                                                                                                                                                                                                                                                                          Score 5; DB 1; ; Pred. No. 1.4e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AA
behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M62812; -; NOT_ANNOTATED_CDS.
Luminescence; Ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                              20.0%;
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                                                                                                                                                                                                                                                                                                                                                                           1; Conservative
                                                                                              Neuropeptide; Amidation.
CHAIN 1 4
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Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio fischeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=668;
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ID _DCMS_PSECH
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MOD_RES
SEQUENCE
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LUXE_VIBFI
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   SPEFFFS
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-!- COFACTOR: Binds 2 2Fe-2S clusters.
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
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MCFATIANE I.D., Hudman D., Nochacker H.-P., Grimmelikhuijzen C.J.D.;
MCFATIANE I.D., Hudman D., Nochacker H.-P., Grimmelikhuijzen C.J.D.;
MCFATIANE I.D., Hudman D., Nochacker H.-P., Grimmelikhuijzen C.J.D.;
Inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
Proc. R. Soc. Lond. Biol. Sci. 253:188-1881(193).
I-FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
I-SUBCELULAR LOCATION: Secreted.
I-TISSUE SPECIFICITY: Neuron specific.
PIR: JO1273; JO1273.
MOD_RES I I. L-3-PHENYLLACTYL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
-!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kraut M., Hugendieck I., Herwig S., Meyer O.; "Homology and distribution of CO dehydrogenase structural genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P., irsolation of L.3-phenyllactyl-phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones. Biochem. Biochys. Res. Commun. 179:1205-1211(1991).
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1993 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO dehydrogenase subunit S) (CO-DH S) (Fragment).
                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae.
NCBI_TaxID=290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; PL0146; PL0146.
Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-28.
NON TER
SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2; DB 1; I
Pred. No. 1.4e+05;
1; Mismatches 0
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90055678; PubMed=2818128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92028852; PubMed=1681803;
                                                                                                                                                                                                                     Pseudomonas carboxydohydrogena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 0.0%;
Matches 0; Conservative
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MOD RES 4 4 AMIDATION.
SEQUENCE 4 AA; 512 MW; 6DD339C9A000000 CRC64;
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0; Gaps Query Match 8.0%; Score 2; DB 1; Length 4; Best Local Similarity 0.0%; Pred. No. 1.4e+05; Matches 0; Conservative 1; Mismatches 0; Indels

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Search completed: September 7, 2004, 19:24:35 Job time : 9 secs

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OM protein

Run on:

Sequence:

Searched:

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008433,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last amotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
Rattus sp. Batazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Sepia officinalis (Common cuttlefish).
Bukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Decapodiformes, Sepioidea, Sepiidae, Sepia.
NCBI_TaxID=6610,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 24.0%; Score 6; DB 5; Length 2; Local Similarity 100.0%; Pred. No. 1e+06; les 1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%; Score 2; DB 11; Length 4; 0.0%; Pred. No. 1e+06; 0; Indels ative 1; Mismatches 0; Indels
                                                                                                 SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION TISSUE=Optic lobe; PubMed=9437704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    Neuropeptide, Amidation.
MOD RES 2 2 AMIDATION.
SEQÜENCE 2 AA; 261 MM; 73781000000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER 1 1 1 SEQUENCE 4 AA; 473 MW; 633732C42000000 CRC64;
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35.058 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
Neuropeptide GWa.
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Perfect score:
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P83570

No. Result

RESULT 1 P83570 ID P8355 AC P8355 AC P8355 DT 01-JI DT 01-JI DE Neuro

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us-09-931-009a-2.closed.rspt

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TISSUE=Egg;

PubMed=12207999;

PubMed=12207999;

A Zatylny C., Marvin L., Gagnon J., Henry J.;

A zatylny C., Marvin E., Gagnon J., Henry J.;

T "Fertilization in Sepia officinalis: the first mollusk sperm-attracting peptide.";

Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).

-!- FUNCTION: HAS XYOTROIT ACTIVITY TARGETING THE GENITAL TRACT.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- TISSUE SPECTROMETRY: FOLLICLE, FULLY GROWN OCCYTE AND EGG(EC2).

-!- MASS SPECTROMETRY: WM=505.4; METHOD=MALDI.

GO; GO:0005186; F:pheromone activity; IEA.
                                                                                                                                                                                                                                                                    SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS SPECTEROMETRY.
TISSUE-EGG;
BubMed=10944467;
Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
"ILME: a waterborne pheromonal peptide released by the eggs of Sepia Officinalis.";
Biochem. Biophys. Res. Commun. 275:217-222(2000).
Pheromone peptide ILME.
Sepia offichnalis (Common cuttlefish).
Bezaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
NCBI_TaxID=6610;
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0.0%; Score 0; DB 5; Length 4;

Best Local Similarity 0.0%; Pred. No. 1e+06;

Matches 0; Conservative 0; Mismatches 1; Indels
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Search completed: September 7, 2004, 19:25:17 Job time : 36 secs

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Sequence 1, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 6, Appli
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Sequence 26, Appli
Sequence 3, Appli
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Sequence 46, Appli
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Sequence 4, P
PCT-US03-07665-1
PCT-US03-21664-1
PCT-US03-301161-1
PCT-US03-301161-1
US-08-138-820-6
US-07-705-27060-6
US-07-705-27060-6
US-08-138-820-1
US-08-138-820-1
US-08-138-820-1
US-08-091-518-5
US-09-091-518-5
US-09-081-15-6
US-09-081-15
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PCT-US03-07665-1
; Sequence 1, Application PC/TUS0307665
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9.385 Million cell updates/sec
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1: /cgn2 6/ptodata/2/paa/USO6 COMB.pep:*
2: /cgn2 6/ptodata/2/paa/USO6 COMB.pep:*
3: /cgn2 6/ptodata/2/paa/USO7 COMB.pep:*
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7: /cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
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14: /cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
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16: /cgn2 6/ptodata/2/paa/USO9 COMB.pep:*
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20: /cgn2 6/
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 65 summaries
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RESULT 4
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GENERAL INFORMATION:
APPLICANT: BRESAGEN, LID.
APPLICANT: MEDICAL COMPOSITIONS AND METHODS FOR ENRICHMENT OF NEURAL STEM
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENRICHMENT OF NEURAL STEM
TITLE OF INVENTION: CELLS USING CERAMIDE ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BRESAGEN, LTD.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL DIFFERENTIATION
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEURAL DIFFERENTIATION
TITLE OF INVENTION: OP EMBRYONIC STEM CELLS
FILE REFERENCE: 18465-0024
CURRENT APPLICATION NUMBER: PCT/US03/24864
CURRENT APPLICATION NUMBER: PCT/US03/24864
CURRENT FILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: US 60/401,968
PRIOR PILING DATE: 2003-03-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN OF SEQ ID NOS: 5
SEG ID NO 1
LENGTH: 4
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                      APPLICANT: BRESAGEN LIMITED
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRIMATE NEURAL CELL
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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PCT-US03-24864-1
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APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
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GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
APPLICANT: BRESAGEN, LTD.
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100.0%; Score 25; DB 1; I
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.5e+06;
                                                                                         CURRENT APPLICATION NUMBER: PCT/US03/07665
CURRENT APPLICATION NUMBER: PCT/US03/07665
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/364,381
PRIOR FILING DATE: 2002-03-13
SOFTWARE OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use CIRRENERMENCE: UNGRALISA CURRENT APPLICATION NUMBER: PCT/US98/27060

CURRENT FILING DATE: 1998-12-17

EARLIER APPLICATION NUMBER: 08/993,165

EARLIER APPLICATION VOMBER: 08/993,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: IMARX PHARMACEUTICAL
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
FILE REFERENCE: UNGRIS36
CURRENT APPLICATION NUMBER: PCT/US98/27060A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
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* OTHER INFORMATION: Description of Artificial Sequence: novel sequence
PCT-US98-27060-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4;
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100.0%; Score 25; DB 1; I
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
FILE REFERENCE: 18377-0024
CURRENT APPLICATION NUMBER: PCT/US03/30112
CURRENT FILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: US 60/413,510
FRIOR FILING DATE: 2002-09-25
FRIOR PELLOR DATE: 2002-09-25
FRIOR FILING DATE: 2003-07-07
NUMBER: OS SEQ ID NOS: 16
SEQ ID NO 1
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: FATER, Michael B.
REGISTRATION NUMBER: 32,612
REFRENCE/POCKET NUMBER: 3045
TELECOMMUNICATION: TELECOMMUNICATION: TELEPHONE: (310) 445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (310) 445-9031
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       Collegeville
PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                      USA
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; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence PCT-US98-27060-6
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APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSS:
ADDRESSES: TILLON, FALLON, LUNGMUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08138820
GENERAL INFORMATION:
APPLICANT: Klein, Scott I.
TITLE OF INVENTION: ANTITHROMEOTIC AZACYCLOALKYLALKANOYL.
TITLE OF INVENTION: PEPTIDES AND PSEUDOPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 3; Length 4; 100.0%; Pred. No. 5.5e+06;
                                                                        100.0%; Score 25; DB 1; Length 4; 100.0%; Pred. No. 5.5e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPREY: USA

ZIP: 66064-4002

ZIP: 66066-4002

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUFTWARE: Patentin Release #1.0, Version #1.25
SURRENT SPELICATION DATA:
APPLICATION NUMBER: US/07/705,071
FILING DATE: 19910624
CLASSIFICATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033
TELEPHONE: 312/456-9000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
ITYPE: AMINO ACID
STRANDEDNESS: unknown
STRANDEDNESS: unknown
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Best Local Similarity 100.
Matches 4; Conservative
                                                                          Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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STATE: ILLINOIS
COUNTRY: USA
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US-08-138-820-4
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Gaps
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US-08-26-9
US-0
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
ZIP: 19426
COUNTYER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (Patentin)
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/08/138,820
FILING DATE: 15-OCT-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Darkes, Paul R.
REGISTRATION NUMBER: 33,862
REFERENCE/DOCKET NUMBER: A1158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TURDER: Amino acids
TURDER: Amino acids
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ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Bush, Larry R
APPLICANT: Swenson, Stephen
APPLICANT: Sanchez, Eladio F
IITLE OF INVENTION: Thrombolytic Agents with Antithrombotic
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 25; DB 11; Length 4; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          h similarity 100.0%; Score 25; DB 6; Length 4; Similarity 100.0%; Pred. No. 5.5e+06; 4; Conservative 0; Mismatches n: Tahale
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MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentlN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,781B
FILING DATE:
PILING DATE: 02-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGRIT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,2056
TELECOMMUNICATION INFORMATION:
TELEPHAN: 312 913 0002
TELEFPAX: 312 913 0002
                                                                                                                                                                                       ; ORGANISM: Ligand sequence recognized by integrin US-08-260-514-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08753781B GENERAL INFORMATION:
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                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                 internal
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                                        : 4 amino acids amino acids
                    SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-753-781B-2
                                          LENGTH:
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0
                                                  APPLICANT: Markland Jr., Francis S.
APPLICANT: Bush, Larry R.
APPLICANT: Swenson, Stephen
APPLICANT: Flores Sanchez, Eladio
TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC
TITLE OF INVENTION: ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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APPLICANT: Lee, Theodore T.
APPLICANT: Ratnikov, Boris I.
APPLICANT: Ratnikov, Boris I.
APPLICANT: Ratnikov, Boris I.
APPLICANT: Smith, Jeffrey W.
IITLE OF INVENTION: AGGLUTRIMETRIC ASSAYS IN BLOOD
FILE OF INVENTION: AGGLUTRIMETRIC ASSAYS IN BLOOD
FILE REPERSICE: 25608-001401
CURRENT APPLICATION NUMBER: US/09/040,712
CURRENT FILING DATE: 1998-03-18
PRIOR APPLICATION NUMBER: US 08/820,999
PRIOR PILING DATE: 1997-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/982,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 13;
Pred. No. 5.5e+06;
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100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 5.5
Matches 4; Conservative 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/753,781
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MCDAILEIS, PALTICIA A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI
TELECOMMUNICATION INFORMATION:
TELEPAX: 603 437 8970
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09040712 GENERAL INFORMATION:
Sequence 1, Application US/08982981
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
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us-09-931-009a-2.open.rapm

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Sequence 2, Application US/09376529 GENERAL INFORMATION:
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                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
    PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
COTHER INFORMATION: Unknown US-09-376-529-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                 Best_Local Similarity
Matches 4; Conserv
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Best Local Similarity
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US-09-376-529-2
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US-09-593-117-6
  SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                   Query Match
                                              LENGTH
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APPLICANT: Shen, Dekang
APPLICANT: W. Guanlı
TITLE OF INVENTION: Novel Targeted Compositions For Diagnostics And
TITLE OF INVENTION: Therapeutic Use
FILE REFERENCE: DUP-0307
CURRENT APPLICATION NUMBER: US/09/218,660
CURRENT FILING DATE: 1998-12-22
FRIOR APPLICATION NUMBER: 08/660,032
PRIOR FILING DATE: 1996-06-06
PRIOR FILING DATE: 1996-06-01
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-091-578B-5

Sequence 5, Application US/09091578B

GENERAL INFORMATION:

APPLICANT: MADISON, EDMIN L.

APPLICANT: MADISON, EDMIN L.

TITLE OF INVENTION: TARGETED THERAPEUTIC OR DIAGNOSTIC

TITLE OF INVENTION: AGENTS AND METHODS OF MAKING AND USING SAME

FILE REFERENCE: 19191.000

CURRENT APPLICATION NUMBER: US/09/091,578B

CURRENT APPLICATION NUMBER: PCT/US96/20577

PRIOR PALLICATION NUMBER: ECT/US96/20577

PRIOR PLILING DATE: 1996-12-19

PRIOR PLILING DATE: 1995-12-21

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FASTSEQ FOR Windows Version 4.0

SEQ ID NO 5

LENGTH: 4
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                                                            FEATURE:
COTHER INFORMATION: GPRP Peptide
LOCATION: (1)..(4)
COTHER INFORMATION: Peptide inhibitor of fibrin polymerization.
US-09-040-712-3
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; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence; Note

; OTHER INFORMATION: artificial construct

US-09-091-578B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 14; Length 4; 100.0%; Pred. No. 5.5e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                   Query Match 100.0%; Score 25; DB 14; Length 4; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 4; Conservative 0; Mismatches 0; Indels
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LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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APPLICANT: Evan C., Unger
APPLICANT: Evan C., Unger
APPLICANT: Wan, Yungiu
TILE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
FILE REFERENCE: UNGRI594
CURRENT FILING DATE: 1097-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH A.
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; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence US-09-218-660-4
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SOFTWARE: FastSEQ for Windows DEMONSTRATION Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 17;
100.0%; Pred. No. 5.5e+06;
cive 0; Mismatches 0;
                                                                     100.0%; Score 25; DB 16; 100.0%; Pred. No. 5.5e+06;
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Pred. No. 5.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thakur, Madhukar L.
TITLE OF INVENTION: Imaging With TC-99 Labeled
TITLE OF INVENTION: Fibrin-Alpha-Chain Peptide
FILE REPERENCE: THAO1.NPO03
CURRENT APPLICATION NUMBER: US/09/376,529
CURRENT APPLICATION NUMBER: US/09/376,529
FRIOR REPLICATION NUMBER: 60/096,803
FRIOR FILING DATE: 1998-08-17
                                                                                                                      0; Mismatches
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; OTHER INFORMATION: Synthetic construct
US-09-593-117-6
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APPLICANT: Under, Evan C.
APPLICANT: Shen, Dekang
APPLICANT: Widner, Cauani
TITLE OF INVENTION: NOVel Targeted Compositions For Diagostics And Therapeutic Use
FILE REFERENCE: UNGRIS98
FULNE APPLICATION NUMBER: US/09/699,679A
CURRENT FILING DATE: 1998-12-22
FRIOR FILING DATE: 1996-06-06
FRIOR FILING DATE: 1996-05-01
FRIOR FILING DATE: 1996-05-01
FRIOR FILING DATE: 1996-06-07
FRIOR PRICE FILING DATE: 1996-06-07
FRIOR FILING DATE: 1996-06-07
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) OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

US-09-687-156A-1
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TILLE OF INVENTION: Imaging with TC-99m Labeled Fibrin Alpha
TITLE OF INVENTION: Chain Peptide
TITLE OF INVENTION: Chain Peptide
FILE REFERENCE: 8321-119
CURRENT APPLICATION NUMBER: US/09/763,777B
CURRENT FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: US 60/096,803
PRIOR APPLICATION NUMBER: US 60/096,803
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 25; DB 20; Length 4; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 25; DB 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-699-679A-4
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APPLICANT: Sherbine, James P.
APPLICANT: Sherbine, James P.
APPLICANT: Sledeski, Adam W.
TITLE OF INVENTION: STABLE NOW-HYGROSCOPIC CRYSTALLINE FORM OF N-[N-[N-(4-(PIPERIDIN-TITLE OF INVENTION: YL) BUTANOYL) -N-ETHYLGLYCYL] ASPARTYL] -L-BETA-CYCLCHEXYL ALANINE ATITLE OF INVENTION: INTERMEDIATES THEREOF, AND PREPARATION THEREOF AND OF ANTITHROME FILE REFERENCE: A2234B US
CURRENT APPLICATION NUMBER: US/09/639,634A
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) FEATURE:

OTHER INFORMATION: Synthetic peptide capable of inhibiting binding of fibrinogen to

) OTHER INFORMATION: platelets
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US-09-687-156A-1

SGQUENCE 1. Application US/09687156A

SGRUENCAL INFORMATION:

APPLICANT: Thaler, David S

APPLICANT: Messmer, Bradley T

TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS

TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING

FILE REPERENCE: 600-1-262N

CURRENT PRILIG DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 91
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         Indels
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100.0%; Score 25; DB 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
      Mismatches
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PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: PCT/US97/14756
PRIOR FILING DATE: 1997-08-21
PRIOR APPLICATION NUMBER: 60/024,284
PRIOR FILING DATE: 1996-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salazar , Diane (Deceased)
Salazar , Richard (Legal)
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Aventis Pharmaceuticals Inc. APPLICANT: Chrzan, Zofia J
                                                                                                                                                                                                                                                                                                                                                                            Chrzan, Zofia J
Mencel, James J
Toledo-Valasquez, David
Windisch, Vincent
Woodward, Rick G
                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09639634A GENERAL INFORMATION:
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Gardetto, Anthony J.
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SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matthew, Powers R. Kubiak, Gregory G.
   4; Conservative
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1 GPRP 4
                                                                     1 GPRP 4
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      Matches
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APPLICANT: Way, Shih-Kwang
APPLICANT: Tseng, Chin-Lu
APPLICANT: Tseng, Chin-Lu
APPLICANT: Tseng, Chin-Lu
APPLICANT: Chang, Ting-Gung
APPLICANT: Chin, Kea-Shyang
APPLICANT: Shih, Kea-Shyang
APPLICANT: Chingates Synthesized Thereby and Targeted Liposomes Containing
TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
FILE REFERENCE: P1379
CURRENT APPLICATION NUMBER: US/10/016,569A
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.2
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; OTHER INFORMATION: Unknown. Obtained from a commercial source.
US-09-931-009A-2
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                                                                                                                                                               US-09-931-009A-2
SEQUENCE 2, ADDICATION US/09931009A
GENERAL INFORMATION:
APPLICANT: SMAICH, Theresa H.
TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE
FILE REFERENCE: US 1257/01 (VA)
CURRENT APPLICATION NUMBER: US/09/931,009A
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 26;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human Cell
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1 GPRP 4
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1 GPRP 4
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US-10-046-801-6
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US-09-813-484-6
Sequence 6, Application US/09813484
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TITLE OF INVENTION: Novel Methods Of Ultrasound Treatment Using Gas Or Gaseous Precur
TITLE OF INVENTION: Novel Methods Of Ultrasound Treatment Using Gas Or Gaseous Precur
TITLE OF INVENTION: NOVEL Methods Of Ultrasound Treatment Using Gas Or Gaseous Precur
TITLE OF INVENTION: VANDER: US/09/813,484
CURRENT FILING DATE: 1001-03-21
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Version 3.1
SEQ ID NO 6
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
US-09-779-054-16
US-09-779-054-16
Squence 16, Application US/09779054
GGENERAL INFORMATION:
APPLICANT: Lu, Xinjie
APPLICANT: Kakar, Vijay
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT RAPLICATION WUMBER: US/09/779,054
CURRENT PILING DATE: 2001-02-05
PRIOR PPLICATION WUMBER: GB 0002625.2
PRIOR PILING DATE: 2000-02-05
NUMBER OF SEQ ID NOS: 21
SSOTUMARE: Patentin version 3.0
LENGTH: 4
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                                                                     FEATURE:
OTHER INFORMATION: Analog of N-terminus tripeptide identified in SEQ
OTHER INFORMATION: ID NO: 1
US-08-763-778-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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100.0%; Score 25; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                Length 4;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                           100.0%; Score 25; DB 22;
100.0%; Pred. No. 5.5e+06;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: thrombin-binding sequence US-09-779-054-16
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity luv...
4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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ORGANISM: Artificial
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FEATURE:
) OTHER INFORMATION: Description of Artificial Sequence: Synthetic
IS OTHER INFORMATION: peptide
US-10-674-756-9
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US-08-085-126-76
Squence Application US/08085126
; Sequence To Application US/08085126
; GENERAL INFORMATION:
    APPLICANT: LADNER, Robert C.
    APPLICANT: CANNON, LATICK E.
    TITLE OF INVENTION: THERFORE
    NUMBER OF SEQUENCES: 236
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: BROWN AND NEIMARK
    STREET: 419 Seventh Street, N.W.
    CITTY Washington
    STATE: D.C.
    COUNTRY: USA
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                                                                                                           Length 4;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/085,126
FILING DATE: 25-UNW-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LADNER=10
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION INFORMATION:
TELEPASS: 202-737-3528
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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US-08-438-114-76
Sequence 76, Application US/08438114
GENERAL INFORMATION:
TANNER Pichard C.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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amino acid
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APPLICANT: CANNON, LAD
TITLE OF INVENTION: CF
TITLE OF INVENTION: TF
NUMBER OF SEQUENCES: 2
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APPLICANT: Tseng, Chin-Lu
APPLICANT: Tseng, Chin-Lu
APPLICANT: Chang, Thig-Gung
APPLICANT: Chang, Thig-Gung
APPLICANT: Chang, Thig-Gung
APPLICANT: Chen, Li-Jung
APPLICANT: Shih, Kea-Shyang
TITLE OF INVENTION: Solid Phase Method for Synthesis Peptide-Spacer-Lipid Conjugates,
TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing
FILE REFERENCE: P1379
CURRENT APPLICATION NUMBER: US/10/308,644
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
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; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-10-046-801-6
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Sequence 9, Application US/10674756;
GENERAL INPORMATION:
APPLICANT: FORWOOD, JADE KENNETH
APPLICANT: MORRIS, MICHAEL BRADLEY
TITLE OF INVENTION: RECEPTOR EXPRESSED IN PLURIPOTENT CELLS
FILE REFERENCE: 18377-0025
CURRENT APPLICATION NUMBER: US/10/674,756
CURRENT APPLICATION NUMBER: US/10/674,756
PRIOR FILING DATE: 2003-09-30
PRIOR FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 4
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100.0%; Score 25; DB 26;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US/09/540,448
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 1997-09-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 4
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Sequence 25, Application US/10308644
GENERAL INFORMATION:
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                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Human Cell
US-10-308-644-25
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US-10-674-756-9
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APPLICANT: Robert, Koll
APPLICANT: Richter, W.
APPLICANT: Bieber, Franz
APPLICANT: Bieber, Franz
APPLICANT: Tschoppe, W.
TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS. 1328/2
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100.0%; Score 25; DB 18;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.5e+06;
tive 0; Mismatches 0;
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APPLICANT: Richter, W.
APPLICANT: Bieber, Franz
APPLICANT: Bieber, Franz
ITILE OF INVENTION: AGENT FOR THE TREATMENT AN
ITILE OF INVENTION NUMBER: US/09/462,446A
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SECTION: AGENT AND AGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/462,446A CURRENT FILING DATE: 2000-06-05 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin version 3.0 SOFTWARE: Patentin version 3.0
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LOCATION: (1)...(5)
OTHER INFORMATION: X is any amino acid
NAME/KEY: PEPTIDE
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CTHER INFORMATION: Synthesized Peptide US-09-462-446A-1
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; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Synthesized Peptide
US-09-462-446A-2
                                                                                                                                                                                                                                                                                             US-09-462-446A-1; Sequence 1, Application US/09462446A; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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1 GPRP 4
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US-09-462-446A-2
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US-09-376-529-3
US-09-376-529-3
SEQUENCE 3, Application US/09376529
GENERAL INFORMATION:
APPLICANT: Thack! Madhukar L.
ITILE OF INVENTION: Imaging With TC-99 Labeled
ITILE OF INVENTION: Fibrin-Alpha-Chain Peptide
FILE REPERBENCE: THAQ1.NPO03
CURRENT FILING DATE: 1999-08-18
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows DEMONSTRATION Version 4.0
SEQ ID NO 3
LENGTH: 5
TUNNELLY SECTION OF SET SEQ ID NOS: 5
SEQ ID NO 3
TENDER OF SEQ ID NOS: 5
TUNNELLY SECTION OF SECTION OF SEQ ID NOS: 5
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TUNNELLY SECTION OF S
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                                                                                                                                                                                                                                                                   COMPUTER ENDAMBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,114
FILING DATE: US-08-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,793
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/085,126
FILING DATE: 25-JUN-1993
ATTONEY/AGENT INPORMATION:
NAME: COOPER, IVER P:
REGISTRATION NUMBER: Z8,005
REGISTRATION NUMBER: Z8,005
REBERENCE/DOCKET NUMBER: LADNER-10B
TELERRAK: 202-737-3528
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0; Mismatches 0;
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 100.0%; Score 25; Similarity 100.0%; Pred. No. 5 4; Conservative 0; Mismatche
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ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Unknown
US-09-376-529-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                STREET: 412
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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1 GPRP 4
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OTHER INFORMATION: Pentapeptide analog related to N-terminus portion
OTHER INFORMATION: of fibrin-alpha-chain peptide
US-09-763-7779-3
      Sequence 3, Application US/09763777B;
GENERAL INPORMATION:
APPLICANT: Thakur, Madhikar (Matthew) L.
TITLE OF INVENTION: Imaging with TC-99m Labeled Fibrin Alpha
TITLE OF INVENTION: Chain Peptide
TITLE OF INVENTION: Chain Peptide
CURRENT APPLICATION NUMBER: US/09/763,777B;
FILE REFERENCE: 1999-08-17
PRIOR APPLICATION NUMBER: DCT/US99/19011
PRIOR APPLICATION NUMBER: US 60/096,803
PRIOR FILING DATE: 1998-08-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           h Similarity 100.0%; Score 25; DB 22; Length 5; Similarity 100.0%; Pred. No. 5.5e+06; 4; Conservative 0; Mismatches 0; Indels
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COUNTRY: USA
ZIP: 94701-1986
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Buetner, Joseph A.
APPLICANT: Buetner, Joseph A.
Baumbach, George A.
Hammond, David J.
TITLE OF INVENTION: Fibrinogen Binding Peptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSED: Bayer Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Giblin, James A. REGISTRATION NUMBER: 25772 REFERENCE/DOCKET NUMBER: MSB-7233 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (510) 705-7910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 800 Dwight Way
P. O. Box 1986
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Berkeley
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Best Local Similarity
Matches 4; Conserv
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JS-09-763-777B-3
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US-09-953-657-4
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APPLICANT: Robert, Koll
APPLICANT: Richter, W.
APPLICANT: Bieber, Fanz
APPLICANT: Bieber, Fanz
APPLICANT: Tschoppe, W.
TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
FILE REPERRORS: ALCOPATION NUMBER: US/10/619,520
CURRENT APPLICATION NUMBER: US/10/619,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NOTE:
APPLICANT: Richter, W.
APPLICANT: Richter, W.
APPLICANT: Richter, W.
APPLICANT: Bieber, Franz
APPLICANT: Bieber, Franz
APPLICANT: Seber, Pranz
APPLICANT: Seber, Por THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
TITLE OF INVENTION: AGENT FOR THE TREATMENT AND/OR PROPHYLAXIS OF MICROCIRCULATORY DIS
FILE REFERENCE: Attorney Docket No. 1328/2
CURRENT FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 8
SEQ ID NO I
ENGTH: 5
LENGTH: 5
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100.0%; Score 25, DB 25;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.5e+06;
cive 0; Mismatches 0;
                                                                                           DATE: 28-JUN-1990
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-953-657-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
LOCATTON: (1)..(5)
OTHER INFORMATION: X is any amino acid
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: Synthesized Peptide
US-10-619-520-1
TELEFAX: (510)705-7904
JOURNAL: Thromb. Haemost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10619520
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 5
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
                                                                                        439-444
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                                            VOLUME:
ISSUE:
PAGES:
DATE:
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TILE OF INVENTION: PLASYA PROTEIN-BINDING LIGANDS
FILT EFFERENCE: 221948
CURRENT APPLICATION NUMBER: US/10/414,524
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: 60/372,091
PRIOR FILING DATE: 2002-04-15
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 25; DB 30; Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 28, Application US/10414524
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-414-523-23
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APPLICANT: Moss, Marcia Lynn
APPLICANT: Rasmussen, Fred H.
APPLICANT: Vitek, Michael P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic US-10-414-524-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GPRP 4
                                         1 GPRP
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US-10-414-524-28
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TITLE OF INVENTION: METHOD FOR DETECTING LIGANDS AND TARGETS IN A MIXTURE
FILE REFERENCE: 221007
CURRENT APPLICATION NUMBER: PCT/US03/11799
CURRENT FILING DATE: 2003-04-14
PRIOR FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 6
LENGTH: 6
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Sequence 28, Application PC/TUS0311798

GENERAL INFORMATION:

APPLICANT: American National Red Cross

TITLE OF INVENTION: PLASMA PROTEIN-BINDING LIGANDS

FILE REFERENCE: 221947

CURRENT APPLICATION NUMBER: PCT/US03/11798

CURRENT PILING DATE: 2003-04-14

PRIOR APPLICATION NUMBER: 60/372,091

PRIOR PILING DATE: 2002-04-15

NUMBER OF SEQ ID NOS: 119

SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                           100.0%; Score 25; DB 31;
100.0%; Pred. No. 5.5e+06;
ative 0; Mismatches 0;
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                                                                                  NAME/KEY: PEPTIDE
J. COCATION: (1)..(5)
OTHER INFORMATION: Synthesized Peptide
US-10-619-520-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US03-11799-23; Sequence 23, Application PC/TUS0311799; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
COTHER INFORMATION: Synthetic PCT-US03-11799-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic PCT-US03-11798-28
                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 4; Conserv
                                           LOCATION: (1)..(5)
FEATURE:
FEATURE:
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPRP 4
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hammond, David J.

TILLE OF INVENTION: METHOD FOR DETECTING LIGANDS AND TARGETS IN A MIXTURE FILE REFERENCE: 221429

CURRENT ILLING DATE: 2003-04-14

PRIOR APPLICATION NUMBER: US/10/414,523

CURRENT APPLICATION NUMBER: US/003-04-14

PRIOR FILING DATE: 2002-04-15

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.2

ISBOIL NO 23
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RESULT 45
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TITLE OF INVENTION: Assays for measuring matrix metalloproteinase activities FILE REFERENCE: 56816-5001-400

CURRENT APPLICATION NUMBER: PCT/US03/17245

CURRENT FILING DATE: 2003-06-02

PRIOR APPLICATION NUMBER: US 60/384,135

PRIOR FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.2

SEQ ID NO 14

LENGTH: 7
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GENERAL INFORMATION:
Sequence 4, Application US/09687156A
GENERAL INFORMATION:
APPLICANT: Thaler, David S
APPLICANT: Massner, Badley T
TITLE OF INVENTION: BUXTURES BY INTERACTIVE PANNING AND BLOCKING
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
CURRENT APPLICATION NUMBER: US/09/687,156A
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS-09-687-156A-3
IS-09-687-156A-3
Sequence 3, Application US/09687156A
GENERAL INFORMATION:
APPLICANT: Thaler, David S
APPLICANT: Messmer, Bradley T
ITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
FILE REFERENCE: 600-1-262N
FILE REFERENCE: 2000-10-13
NUMBER OF SEQ ID NOS: 91
SCOFTWARE PARENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 3
LENGTH: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
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100.0%; Score 25, DB 1, I
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                        TYPE: PRT: ORGANISM: Artificial GRANISM: Artificial FEATURE: FEATURE: THER INFORMATION: metalloproteinase substrate PCT-US03-17245-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 100..
4; Conservative
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GENERAL INFORMATION:
APPLICANT: Thaler, David S
APPLICANT: MESSMER, BETAGLEY T
TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LICANDS IN HETEROGENEOUS
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
CURRENT APPLICATION NUMBER: US/09/687,156A
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5.
BIRNGTH: 7
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GENERAL INFORMATION:
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APPLICANT: Thale of the sequence of the se
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-687-156A-4
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100.0%; Score 25; DB 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
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Gaps

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NSG-687-156A-10

Sequence 10, Application US/09687156A

GENERAL INFORMATION:

APPLICANT: Thaler, David s

TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS

TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS

TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS

TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGAND BLOCKING

CURRENT APPLICATION NUMBER: US/09/687,156A

CURRENT PILLING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 210

SOFTWARE: PATENTIN VET. 2.0
                  TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-9
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Best Local Similarity 100.0%; Pred. No. 5.5e+06; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                            100.0%; Score 25; DB 20;
100.0%; Pred. No. 5.5e+06;
ative 0; Mismatches 0;
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100.0%; Score 25; DB 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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LENGTH: 7
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GENERAL INFORMATION:
APPLICANT: Thaler, David S
APPLICANT: Messmer, Bradley T
TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
FILLE REPERENCE: 600-1-22N
CURRENT APPLICATION NUMBER: US/09/687,156A
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
APPLICANT: Thaler, David s
APPLICANT: Thaler, David s
APPLICANT: Messmer, Bradley T
ITILE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
TITLE REFERENCE: 6001-122N
CURRENT APPLICATION NUMBER: US/09/687,156A
NUMBER OF SEQ ID NOS: 91
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 9
  Sequence 7, Application US/09687156A
GENERAL INFORMATION:
APPLICANT: Thaler, David S
APPLICANT: Mesamer, Bradley T
TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
FILE REFERENCE: 600-1-262N
CURRENT APPLICATION NUMBER: US/09/687,156A
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 7
IENDETH: 7
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, OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-687-156A-8
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Matches 4; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-687-156A-7
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APPLICANT: Thaler, David S
APPLICANT: Thaler, David S
APPLICANT: Thaler, David S
APPLICANT: Thaler, David S
APPLICANT: MESSNER, Bradley T
TITLE OF INVENTION: SEQUENTIAL DETERMINATION OF LIGANDS IN HETEROGENEOUS
TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING
FILE REFERENCE: 600-1-262N
CURRENT APPLICATION NUMBER: US/09/687,156A
NUMBER OF SEQ ID NOS: 91
SCOTWARET FILING DATE: 2000-10-13
NUMBER PALENT FILING DATE: 2000-10-13
SEQ ID NO: 1
LENGTH: 7
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-687-156A-10
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RESULT 50

US-09-687-156A-12

SQUENCE 12, Application US/09687156A

GENERAL INFORMATION:

APPLICANT: Thaler, David S

APPLICANT: Messmer, Baradley T

TITLE OF INVENTION: MIXTURES BY INTERACTIVE PANNING AND BLOCKING

FILE REPERBENCE: 600-1-262N

CURRENT APPLICATION NUMBER: US/09/687,156A

CURRENT BILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 91

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FRATURE:

ORGANISM: Artificial Sequence

FRATURE:

ORGANISM: Altificial Sequence

SEATURE:

GREAT INFORMATION: Description of Artificial Sequence: SYNTHETIC

US-09-687-156A-12

Query Match

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: September 7, 2004, 19:09:11 Job time : 418 secs

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Sequence 64, Appl
Sequence 64, Appl
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Sequence 84, Appl
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Sequence 86, Appl
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                                                                                                                         September 7, 2004, 18:58:53 ; Search time 60 Seconds (without alignments) 8.622 Million cell updates/sec
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1: /cgn2 6/ptodata/2/paa/PCT NEW COMB.pep:*

2: /cgn2 6/ptodata/2/paa/USO6 NEW COMB.pep:*

4: /cgn2 6/ptodata/2/paa/USO7 NEW COMB.pep:*

5: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

5: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

6: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

7: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-USO3-40762-1
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PCT-BR03-00192A-110
PCT-BR03-00192A-246
PCT-BR03-00192A-246
PCT-BR03-00192A-246
PCT-BR03-00192A-248
US-10-459-030B-68
US-10-459-030B-68
US-10-459-030B-76
US-10-459-030B-76
US-10-459-030B-76
US-10-459-030B-76
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PCT-BR03-00192A-534
PCT-BR03-00192A-540
PCT-BR03-00192A-546
US-10-459-030B-92
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Maximum Match 100%
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Match Length DB
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Perfect score:
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27	25	100.0	13	9	US-10-459-030B-112	Sequence 112, App
28	25		14	9	US-10-782-269-6	equence 6,
50	25	-	14	9	US-10-782-269-7	е 7,
30	25		14	9	S-10-459-030B-1	equence 110
31	25		14.	9	-10-459-030B-12	equence 12(
32	25	100.0	12	9	-10-487-886-11	e 11
33	25			ø	-10-459-030B-12	equence 124
34	25		12	φ	10-459-030B-12	equence 128
35	22			φ	-10-459-030B-13	13
36	25		16	9	-10~459-030B-13	136
37	25		17	φ	-10-459-030B-14	140,
38	25		17	ω	10-459-030B-1	144,
39	25		18	ø	-10-459-030B-14	148,
40	25		8	9	-10-459-030B-15	152,
41	25		18	φ	-10-897	37,
42	25		18	v	0-897	38,
43	25		18	9	-10-729	37,
44	25		78	9	-10-729-441-38	œ
45	25		19	9	10-459-030B-15	156,
46	25		19	w	-10-459-030B-1	160,
47	25		20	9	-10-459-030B-16	164,
48	25		20	ø	-10-459-030B-16	168,
49	25		50	9	-10-776-013-598	598,
20	25		21	ເກ	-09-833-245A-55	551,
51	25		21	v	-10-100-683-963	9638
52	25		21	ø	-10-459-030B-17	172,
53	25		21	φ	59-030B-17	176,
54	25		22	v	-10-459-030B-18	180,
55	25		22	φ	-10-459-030B-18	184,
29	25		23	w	10-459-030B-18	188
57	25		23	φ	-10-459-030B-	192,
28	25		24	Ŋ	-09-952-432C-	equence 5, Ap
26	25		24	ø	-10-459-030B-1	equence 196,
9	25	00	24	vo	-10-459-030B-	200
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62) C	000	2.4	v	-10-660-811A-2	equence 249.
9 6	0 10	9	20	·	-10-459-030B-2	emience 204.
9 6) (000	2.5	y C	-10-459-030B-2	equence 208.
65	2 5	100.0	25	w	-10-868-184A-32	ednence
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RESULT 1 PCT-11S04-10121		-				
	e 1, A	Application		TUS	PC/TUS0410121	
GENERAL INFORMATION	INFOR	MATION:				
APPLICANT:		BKESAGEN IN	; 5	Ę	MOTHER CHARGE HOUSE BORNE AT DECEM-	Chi
TITI	OF TMI	TANTENTION		ם מפ	RITO AL DIRE	
		MARKET CON :		;	NOTIFICIANS AND SECURITY OF CALCULATION OF CALCULAT	OF BRIDGIOLOGIC

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PCT-USO4-10121.

Sequence 1. Application PC/TUS0410121
Sequence 1. Application PC/TUS0410121
APPLICANT: BRESAGENING.
APPLICANT: BRESAGENING.
APPLICANT: BRESAGENING.
TITLE OF INVENTION: METHODS FOR NEURAL DIFFERENTIATION OF EMBRYONIC STEM
TITLE OF INVENTION: CELLS USING PROTEASE PASSAGING TECHNIQUES
TITLE OF INVENTION: CELLS USING PROTEASE PASSAGING TECHNIQUES
TITLE OF INVENTION: DATE: 2004-03-31
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: 60/459,090
PRIOR PILING DATE: 2003-03-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTING DATE: 2003-03-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTING DATE: 2003-03-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTING DATE: 2003-03-31
OCAGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: polypeptide
PCT-US04-10121-1
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Sequence

US-10-459-030B-104 US-10-459-030B-108

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid
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100.0%; Pred. No. 6.2e+05;
iive 0; Mismatches 0;
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  APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-BR03-00192A-111; Sequence 111, Application PC/TBR0300192A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 110, Application PC/TBR0300192A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Bothrops jararaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Bothrops jararaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat_peptide
LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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GENERAL INFORMATION:
APPLICANT: BERSAGEN; INC.
APPLICANT: BERSAGEN; INC.
APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
APPLICANTION: STABILIZATION
FILE OF INVENTION: STABILIZATION
FILE OF INVENTION: STABILIZATION
FILE REPRENCE: 18377-0028
CURRENT APPLICATION NUMBER: PCT/US03/40762
PRIOR FILING DATE: 2002-12-18
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PALENTIN Ver. 3.2
SEQ ID NO 1
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                                                                                                                                                                         APPLICANT: University of Texas
TILE OF INVENTION: Micropositioning Cells for Tissue
TILLE OF INVENTION: Engineering
FILE REFERENCE: 2110S.0003P1
CURRENT APPLICATION NUMBER: PCT/USO4/16828
CURRENT FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: 60474,574
PRIOR FILING DATE: 2003-05-30
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 1; L
100.0%; Pred. No. 6.2e+05;
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; Sequence 109, Application PC/TBR0300192A
; GENERAL INFORMATION:
                                                                                                            PCT-US04-16828-4; Sequence 4, Application PC/TUS0416828; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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1 GPRP 4
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PCT-US03-40762-1
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TITLE OF INVENTION: Pharmaceutical Compositions Preparation of Peptides,
TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particulary Of Bothrops jarativite OF INVENTION: Secreted by The Snake Venom Glands, Particulary Of Bothrops jarativite OF INVENTION: Asopoeptidases Inhibitors, Evashis, Their Analogues, Derivatives TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Aplications FILE REPERBNCE: B10205449-3
CURRENT FILING DATE: 2003-12-09
PRIOR FILING DATE: 2003-12-09
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 594
SEQ ID NO 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particulary Of Bothrops jara:
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TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particulary Of Bothrops jaran
TITLE OF INVENTION: Vasopeptidases Inhibitors, Bvasins, Their Analogues, Derivatives
TITLE OF INVENTION: And Decoducts Associated, Thereof. For Development Of Aplications
TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
TITLE REFERENCE: P10205449-3
CURRENT APPLICATION NUMBER: PCT/BR03/00192A
CURRENT APPLICATION NUMBER: BR P10205449-3
PRIOR APPLICATION NUMBER: BR P10205449-3
NUMBER: OF SEQ ID NOS: 594
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APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
TITLE OF INVENTION: Pacereted by The Snake Venom Glands, Particulary Of Bothrops jaran
TITLE OF INVENTION: Vasopeptidases Inhibitors, Evasins, Their Analogues, Derivatives
TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Applications
TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
FILE REFERENCE: PI0205449-3
CURRENT APPLICATION NUMBER: BC 1003-12-09
REIOR FILING DATE: 2003-12-09
NUMBER OF SEQ ID NOS: 594
SEG ID NO 248
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TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REFERENCE: A35899 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR PILING DATE: 20001-12-07
PRIOR APPLICATION NUMBER: AT 2063/2000
PRIOR PILING DATE: 2000-12-12
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LOCATION: (1)

// OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid

PCT-BR03-00192A-246
                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 1; I
100.0%; Pred. No. 6.2e+05;
iive 0; Mismatches 0;
         FILE REFERENCE: PIO205449-3
CURRENT APPLICATION NUMBER: PCT/BR03/00192A
CURRENT FILING DATE: 2003-12-09
PRIOR APPLICATION NUMBER: BR PIO205449-3
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 594
SEQ ID NO 247
LENGTH: 7
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                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Bothrops jararaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bothrops jararaca
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide LOCATION: (1)
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Best Local Similarity
Matches 4; Conserv
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PCT-BR03-00192A-248
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US-10-459-030B-60
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GENERAL INFORMATION:
APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all
APPLICANT: Biolab Sanus Farmaceutica Compositions Preparation Of Peptides,
TITLE OF INVENTION: Paramaceutical Compositions Preparation Of Peptides,
TITLE DE INVENTION: Secreted by The Snake Venom Glands, Particulary Of Bothrops jara
TITLE OF INVENTION: And Products Associated, Thereof. For Development Of Aplications
FILE REFERENCE: PIO205449-3
CURRENT APPLICATION NUMBER: PCT/BR03/00192A
CURRENT APPLICATION NUMBER: PCT/BR03/00192A
CURRENT PILING DATE: 2003-12-09
PRIOR FILING DATE: 2003-12-09
NUMBER OF SEQ ID NOS: 594
SEQ ID NO 246
LENGTH: 7
         Vasopeptidases Inhibitors, Evasins, Their Analogues, Derivatives
And Products Associated, Thereof. For Development Of Aplications
And Use In Chronic-Degenerative Diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.0%; Score 25; DB 1; Length 6; Similarity 100.0%; Pred. No. 6.2e+05; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1) ...
; OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid PCT-BR03-00192A-111
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TITLE OF INVENTION: Vasopeptidases Inhibitors
TITLE OF INVENTION: And Products Associated,
FILLE OF INVENTION: And Vice in Chronic-Degene;
FILE REFERENCE: P10205449-3
CURRENT APPLICATION WUMBER: PCT/BR03/00192A
CURRENT FILING DATE: 2003-12-09
PRIOR APPLICATION WUMBER: BR P10205449-3
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 594
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                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Bothrops jararaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Bothrops jararaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: mat_peptide
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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PCT-BR03-00192A-247
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                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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1 GPRP 4
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US-10-459-030B-76
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US-10-459-030B-72
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US-10-459-030B-64

US-10-459-030B-64

Sequence 64, Application US/10459030B

Sequence 64, Application US/10459030B

Sequence 64, Application

TOTALE OF INVENTION:

FILE REFERENCE: A35699 FOT USA A 071986.0248

CURRENT APPLICATION NUMBER: US/10/459,030B

CURRENT FILING DATE: 2003-06-11

PRIOR FILING DATE: 2001-12-07

PRIOR FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 296

NUMBER OF SEQ ID NOS: 296

SOSTWARE: PASTSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Petcatablauer, Peter
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REPERENCE: A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR APPLICATION NUMBER: A1 2063/2000
PRIOR PILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: AT 2063/2000
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NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
LENGTH: 7
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                                                                                                                                      OTHER INFORMATION: peptide of formula II
                                                                                                                                                      FEATURE:
NAME/KEY: VARIANT
LOCATION: (6)...(7)
OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (6)...(7)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-64
                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100..
---- 4; Conservative
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Best Local Similarity 100.8
Matches 4; Conservative
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                                                                                 TYPE: PRT
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TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: THERAPEUTIC FIRRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REPERENCE: A35699 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 25; DB 6; L
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 6; L
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 4; Conservative 0; Mismatches 0;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 68 LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: peptide of formula II
FEATURE:
                                                                                                                                                           OTHER INFORMATION: peptide of formula II
                                                                                                                                                                                  FEATURE:
NAME/KEY: VARIANT
DOCATION: (6)...(8)
COTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-68
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LOCATION: (6)...(8)
OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-72
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GENERAL INFORMATION:
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                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Matches
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| Sequence 84, Application US/10459030B
| Sequence 84, Application US/10459030B
| GENERAL INFORMATION:
| APPLICAMY: Petzelbauer, Peter |
| TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF |
| FILE REPREDAGE: A3589 PCT 'USA A 071986.0248 |
| CURRENT APPLICATION NUMBER: US/10/459,030B |
| CURRENT FILING DATE: 2003-06-11 |
| PRIOR FILING DATE: 2001-12-07 |
| PRIOR FILING DATE: 2001-12-07 |
| PRIOR FILING DATE: 2001-12-12 |
| NUMBER OF SEQ ID NOS: 296 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
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SEQUENCE 10 INFORMATION:
APPLICANT: Petzelbauer, Peter
TITLE OF INVENTION:
TITLE OF INVENTION: THERAPEUTIC FIRRIN-DERIVED PEPTIDE AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT PAPLICATION NUMBER: PCT/AT01/00387
PRIOR PILING DATE: 2003-06-11
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastEEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                   Length 9;
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100.0%; Pred. No. 6.2e+05;
7ative 0; Mismatches 0;
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                                                                                 FEATURE:
OTHER INFORMATION: peptide of formula II
FEATURE:
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                                                                                                                                                             COTATION: (6)...(9)
CTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (6)...(9)
OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-80
                   LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 100..
A; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                         NAME/KEY: VARIANT
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SEQ ID NO 76
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PCT-BR03 -00192A-527

FCT-BR03 -00192A-527

FCT-BR03 -00192A-527

GENERAL INFORMATION:

APPLICANT: Biolab Sanus Farmaceutica Ltda.; et all

APPLICANT: Biolab Sanus Farmaceutical Compositions Preparation Of Peptides,

ITILE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,

ITILE OF INVENTION: Vasopeptidases Inhibitors, Evasins, Their Analogues, Derivatives;

ITILE OF INVENTION: And Products Associated, Thereof. For Development Of Aplications;

ITILE OF INVENTION: And Use In Chronic-Degenerative Diseases

FILE REPERBORS: P10205449-3

CURRENT APPLICATION NUMBER: BR P10205449-3

FRIOR APPLICATION NUMBER: BR P10205449-3

FRIOR FILING DATE: 2003-12-09

FRIOR FILING DATE: 2002-12-09

NUMBER OF SEQ ID NOS: 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Petzelbauer, Peter
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REFERENCE: A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: peptide of formula II
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                                                                                                                  FEATURE:
NAME/KEY: VARIANT
LOCATION: (6)...(10)
CTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (6)...(10)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-88
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION: Pharmaceutica Ltda.; et all
TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particulary Of Bothrops jaran
TITLE OF INVENTION: Vasopeptidases Inhibitors. Fassins, Their Analogues, Derivatives
TITLE OF INVENTION: And Droducts Associated, Thereof. For Development Of Aplications
TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
GURRENT APPLICATION NUMBER: PCT/ER03/00192A
CURRENT FILING DATE: 2003-12-09
PRIOR PAPLICATION NUMBER: BR P10205449-3
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 594
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Sequence 92, Application US/10459030B
GREERAL INFORMATION:
GREERAL INFORMATION:
TITLE OF INVERMION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
TILLE PEPERENCE: A35859 PCT USA A 071986.0248
CURRENT PELLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-66-11
PRIOR PEPLICATION NUMBER: PCT/AT01/00387
PRIOR PELLICATION NUMBER: AT 2063/2000
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: AT 2063/2000
PRIOR SPRING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: PASCEC for Windows Version 4.0
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: LOCATION: (1)

: OTHER INNFRMATION: Xaa is a pyrrolidone carboxilic acid

PCT-BR03-00192A-546
                                                                                      OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid
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;; Pred. No. 94;
0; Mismatches
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100.0%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0,
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Best Local Similarity 100.
                           NAME/KEY: mat_peptide LOCATION: (1)
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FEATURE:
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TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
FILE FFERENCE: P10205449-3
CURRENT APPLICATION NUMBER: BT P10205449-3
PRIOR PRILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 594
SEQ ID NO $40
LENGTH: II
TYPE: PRI
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Sequence 534, Application PC/TBR0300192A
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SAPELICANT: BIOLOBA Sanus Farmaceutica Ltda.; et all
TITLE OF INVENTION: Pharmaceutical Compositions Preparation Of Peptides,
TITLE OF INVENTION: Secreted by The Snake Venom Glands, Particulary Of Bothrops jara
TITLE OF INVENTION: Assopetidases Inhibitors, Evasins, Their Analogues, Derivatives
TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
TITLE OF INVENTION: And Use In Chronic-Degenerative Diseases
TITLE OF INVENTION NUMBER: PCT/BR03/00192A
CURRENT PILING DATE: 2003-12-09
PRIOR FILING DATE: 2002-12-09
PRIOR FILING DATE: 2002-12-09
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; OTHER INFORMATION: Xaa is a pyrrolidone carboxilic acid
PCT-BR03-001024-5527
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100.0%; Pred. No. 94;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bothrops jararaca
                                     TYPE: PRT
ORGANISM: Bothrops jararaca
FEATURE:
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SEQ ID NO 534
LENGTH: 11
                                                                                                                                   NAME/KEY: mat_peptide LOCATION: (1)
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Best Local Similarity
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PCT-BR03-00192A-540
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          LENGTH: 11
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APPLICANT: Percalbauer, Peter
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REFERENCE: A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR APPLICATION NUMBER: AT 2063/2000
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE FEALENCE: 296
SOFTWARE: ASSESS FOR Windows Version 4.0
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Sequence 108, Application US/10459030B
GENERAL INFORMATION:
TATLE OF INVENTION: THERAPEUTIC FIREIN-DERIVED PEPTIDE AND USES THEREOF
TITLE OF INVENTION: THERAPEUTIC FIREIN-DERIVED PEPTIDE AND USES THEREOF
FILE REPERENCE: A35859 PCT USA A 071986.0248
CURRENT PELING DATE: 2003-06-11
PRIOR FILING DATE: 2001-12-07
PRIOR PILING DATE: 2001-12-07
PRIOR PILING DATE: 2001-12-12
NUMBER 05 SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                              Query Match 100.0%; Score 25; DB 6; Length 12; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: peptide of formula II
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              ; OTHER INFORMATION: Xaa=any amino acid US-10-459-030B-100
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CTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-104
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LOCATION: (6)...(13)
OTHER INFORMATION: Xaa=any amino acid
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Sequence 104, Application US/10459030B
GENERAL INFORMATION:
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US-10-459-030B-100
i Sequence 100, Application US/10459030B
i GENERAL INFORMATION:
APPLICANT: Petzelbauer, Peter
ITILE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
ITILE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
ITILE REPERBENCE: A35659 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 100
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
US-10-459-030B-96
| Sequence 96, Application US/10459030B
| GENERAL INFORMATION:
| APPLICANT: Petzelbauer, Peter | TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF | TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF | TITLE OF INVENTION NUMBER: US/10/459,030B | CURRENT FILING DATE: 2003-06-11 | PRIOR APPLICATION NUMBER: PCT/AT01/00387 | PRIOR PILING DATE: 2000-12-07 | PRIOR APPLICATION NUMBER: AT 2063/2000 | PRIOR PILING DATE: 2000-12-12 | PRIOR PETING DATE: 2000-12-12 | PRIOR DOS: 296 | PRIOR DOS: 296
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OTHER INFORMATION: peptide of formula II
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OTHER INFORMATION: peptide of formula II
FEATURE:
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; LOCATION: (6)...(11)
; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-92
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 4; Conservative
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LOCATION: (6)...(12)
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Best Local Similarity
Matches 4; Conserv
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RESULT 29
US-10-782-269-7
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                                                                                                                                                                                                                                                                                     Sequence 112, Application US/10459030B

GENERAL INFORMATION:
APPLICANT' PETZELDAUER, PETZEL
TITLE OF INVENTION:
TITLE OF INVENTION: THERAPEBTIC FIRRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REPERENCE: A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR FILING DATE: 2003-6-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR PLING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FSACSEQ for Windows Version 4.0
SOFTWARE: FSACSEQ for Windows Version 4.0
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APPLICANT: LOPEZ-Avila, Viorica
APPLICANT: Hirschberg, David
TITLE OF INVENTION: Methods and compositions for assessing a
TITLE OF INVENTION: sample by MALDI mass spectrometry
FILE REFERENCE: 10031188-1;
CURRENT APPLICATION NUMBER: US/10/782,269
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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100.0%; Score 25; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                  Query Match
100.0%; Score 25; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 25; DB 6; L
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0;
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LOCATION: (6)...(13)
COTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-112
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ORGANISM: Artificial Sequence
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US-10-459-030B-112
US-10-459-030B-108
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Sequence 116, Application US/10459030B

Sequence 116, Application US/10459030B

Sequence 116, Application US/10459030B

TOTAL REPERBAL INFORMATION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF

FILE REPERBANCE: A35869 PCT USA A 071986.0248

FILE REPERBANCE: A35869 PCT USA A 071986.0248

CURRENT APPLICATION NUMBER: ECT/AT01/00387

FRIOR FILING DATE: 2001-12-07

FRIOR FILING DATE: 2000-12-12

FRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 296

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 116
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                                                  APPLICANT: LOPEZ-AVIIA, Viorica
APPLICANT: LOPEZ-AVIIA, Viorica
APPLICANT: LOPEZ-AVIIA, Methoda
TITLE OF INVENTION: Methoda compositions for assessing
TITLE OF INVENTION: Methoda mass spectrometry
FILE REPERENCE: 10031188-1
CURRENT APPLICATION NUMBER: US/10/782,269
CURRENT APPLICATION NUMBER: US/0.218
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 25; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 25; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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LOCATION: (6)...(14)
S. OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-116
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US-10-459-030B-120
; Sequence 120, Application US/10459030B
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US-10-782-269-7
Sequence 7, Application US/10782269 GENERAL INFORMATION:
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ORGANISM: Artificial Seguence
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FEATURE:

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THENOLIS 34
US-10-459-030B-128

Sequence 129, Application US/10459030B

Sequence 129, Application US/10459030B

GENERAL INFORMATION:
TITLE OF INVENTION: THERREDIT FIBRIN-DERIVED PEPTIDE AND USES THEREOF

TITLE OF INVENTION NUMBER: US/10/459,030B

CURRENT PILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/AT01/00387

PRIOR FILING DATE: 2000-12-07

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 296

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 15
APPLICANT: Petzelbauer, Peter TITLE OF INVENTION: THERAPEUTIC FIRRIN-DERIVED PEPTIDE AND USES THEREOF FILE REFERENCE: A35859 PCT USA A 071986.0246 CURRENT APPLICATION NUMBER: US/10/459,030B CURRENT FILING DATE: 2003-06-11 PRIOR APPLICATION NUMBER: PCT/AT01/00387 PRIOR APPLICATION NUMBER: PCT/AT01/00387 PRIOR PILING DATE: 2001-12-07 PRIOR PILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 296 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO: 296
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100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0;
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Similarity 100.0%; Score 25; DB 6;
Similarity 100.0%; Pred. No. 1.3e+02;
4; Conservative 0; Mismatches 0;
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OTHER INFORMATION: peptide of formula II
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OTHER INFORMATION: Xaa=any amino acid
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LOCATION: (6)...(15)
OTHER INFORMATION: Kaa=any amino acid
US-10-459-030B-128
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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US-10-459-030B-132
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              APPLICANT: Petzalbauer, Peter
TITLE OF INVENTION: THERAPETTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REPERBACE: A38589 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR FILING DATE: 2003-06-11
PRIOR FILING DATE: 2001-12-07
PRIOR RILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120
LENGTH: 14
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APPLICANT: Frentzel, Stefan
APPLICANT: Frentzel, Stefan
APPLICANT: Raupmann, Klemens
APPLICANT: Sommer, Remens
APPLICANT: Sommer, Bernd Josef
APPLICANT: Mir, Anis Khusro
TITLE OF INVENTION: NOOR Receptor Homologues and their use
FILE REPERSINE: 432101/A
CURRENT APPLICATION NUMBER: US/10/487,886
PRIOR APPLICATION NUMBER: US 60/315110
PRIOR PILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 15
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COTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-120
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; Sequence 124, Application US/10459030B
; GENERAL INFORMATION:
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; GENERAL INFORMATION:
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LOCATION: (1)..(15)
OTHER INFORMATION: for immunizing
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Best Local Similarity
Matches 4; Conserv
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Query Match
Best Local Similarity
Matches 4; Conserv
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US-10-459-030B-148
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TITLE OF INVENTION: THERAPBUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REFERENCE: A35599 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR PELING DATE: 2001-06-11
PRIOR PELING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 140, Application US/10459030B
; Cantende 140, Application US/10459030B
; APPLICANT: Petzelbauer, Peter
; TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF FILE REFERENCE: A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,0308
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-12-07
PRIOR PILING DATE: 2001-12-07
PRIOR PILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 132
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100.0%; Score 25; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.4e+02;
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; OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-136
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LOCATION: (6)...(16)
CTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-132
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Best Local Similarity 100.
Matches 4; Conservative
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NAME/KEY: VARIANT
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LENGTH: 16
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US-10-49 030B-144

Sequence 144, Application US/10459030B

Sequence 144, Application US/10459030B

GENERAL INFORMATION:
APPLICAMY:
PETERBLICAMY:
FILE REFERENCE: A35859 PCT USA A 071986.0248

CURRENT APPLICATION NUMBER: US/10/459,030B

CURRENT APPLICATION NUMBER: PCT/AT01/00387

PRIOR APPLICATION NUMBER: PCT/AT01/00387

PRIOR APPLICATION NUMBER: 2003-06-11

PRIOR APPLICATION NUMBER: 2003-12-07

NUMBER OF SEQ ID NOS: 296

SOFTWARE: FREESE FOR Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Petcablauer, Peter
TITLE OF INVENTION: THERAPRITIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REFERENCE: A35859 PCT USA A 071986.0248
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100.0%; Score 25; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
FILE REFERENCE: A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTPARE: FastSEQ for Windows Version 4.0
SEQ ID NO 140
LENGTH: 17
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OTHER INFORMATION: Xaa=any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
DOCATION: (6)...(17)
THER INFORMATION: Xaa=any amino acid
US-10-459-030B-140
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8338
CURRENT APPLICATION NUMBER: US/10/897,406
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US/10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE PARENTIN Version 3.1
SEQ ID NO 38
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GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
TITLE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/729,441
CURRENT PILICATION NUMBER: 10/10/390
PRIOR PILING DATE: 2003-12-08
PRIOR PILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOPTWARE: Patentin version 3.2
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100.0%; Score 25; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.5e+02;
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  CURRENT FILING DATE: 2004-07-23
PRIOR PEPLICATION NUMBER: US/10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 37
LENGTH: 18
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                   TYPE: PRT
; ORGANISM: Homo sapiens
US-10-897-406-37
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US-10-897-406-38
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 18
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100.0%; Score 25; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
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GRNERAL INFORMATION:
APPLICANT: ImmunoGen, Inc.
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8338
CURRENT APPLICATION NUMBER: US/10/897,406
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CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT FILING DATE: 2003-06-11
FRIOR APPLICATION NUMBER: PCT/ATC1/00387
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: AT 2063/2000
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 148
LENGTH: 18
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LOCATION: (6)...(18)
COTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-148
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LOCATION: (6)...(18)
OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-152
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Best Local Similarity
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US-10-897-406-37
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SEQ ID NO 164
LENGTH: 20
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FILE REFERENCE: A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/459,030B
CURRENT APPLICATION NUMBER: US/10/459,030B
PRIOR APPLICATION NUMBER: PCT/AT10/10387
PRIOR PILING DATE: 2003-12-07
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SEQ ID NOS: 296
SEG ID NO 156
LENGTH: 19
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GENERAL INFORMATION:
APPLICATE PETCELDAGAGE, PECET
ITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
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                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/729,441
CURRENT FILING DATE: 2003-12-08
PRIOR PILING DATE: 2002-66-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 18
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LOCATION: (6)...(19)
COTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-459-030B-156; Sequence 156, Application US/10459030B; GENERAL INFORMATION:
                                                                             US-10-729-441-38; Sequence 38, Application US/10729441; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserv
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US-10-459-030B-160
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APPLICANT: Petzelbauer, Peter
APPLICANT: Petzelbauer, Peter
TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REPERENCE: A3599 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: US/10/499,0308
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: AT 2063/2000
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: THERAPEUTIC FIBRIN-DERIVED PEPTIDE AND USES THEREOF
FILE REFERENCE: A35859 PCT USA A 071986.0248
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100.0%; Score 25; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0;
FILE REFERENCE: A35859 PCT USA A 071986.0248
CURRENT APPLICATION NUMBER: U3/10/459,030B
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/AT01/00387
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 296
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 160
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: peptide of formula II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: peptide of formula II
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LOCATION: (6)...(20)
OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (6)...(19)
OTHER INFORMATION: Xaa=any amino acid
US-10-459-030B-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-459-030B-164; Sequence 164, Application US/10459030B; GENERAL INFORMATION:
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; Sequence 168, Application US/10459030B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Score 25; DB 5;
Pred. No. 1.8e+02;
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TITLE OP INVENTION: Albumin Fusion Proteins
FILE REPRENCE: PF946
CURRENT APPLICATION NUMBER: US/09/833,245A
CURRENT FILING DATE: 2001-04-12
NUMBER: OF SEQ ID NOS: 2277
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 551
LENGTH: 21
TYPE: PRT
COGRANISM: Homo sapiens
US-09-833-245A-551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: September 7, 2004, 19:10:18 Job time : 61 secs
                                                                                                                                                                 US-09-833-245A-551; Sequence 551, Application US/09833245A; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 4; Conservative
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14 GPRP 17
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GENERAL INFORMATION:
APPLICANT: WRIAD CENETICS, INC.
APPLICANT: RAILO GENETICS, INC.
APPLICANT: RAILO GENETICS, INC.
APPLICANT: Heichman: Karen
APPLICANT: Heichman: Karen
APPLICANT: Heichman: Karen
APPLICANT: Bartel, Paul
APPLICANTON: ONNOBER: US/10/76,013
CURRENT FILING DATE: 2004-02-09
FRIOR PELING DATE: 2004-02-10
FRIOR PELICATION NUMBER: 09/466139
FRIOR PELING DATE: 1999-12-21
FRIOR PELING DATE: 1999-12-22
FRIOR APPLICATION NUMBER: 60/13534
FRIOR PELING DATE: 1999-03-10
FRIOR PELING DATE: 1999-03-10
FRIOR PELING DATE: 1999-03-10
FRIOR PELING DATE: 2001-01-1
FRIOR FILING DATE: 2001-01-1
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100.0%; Score 25; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/459,030B; CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/AT01/00387; PRIOR FILING DATE: 2001-12-07

PRIOR PILING DATE: 2001-12-07

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 296

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: peptide of formula II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Xaa=any amino acid US-10-459-030B-168
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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SOFTWARE: Patentin version
SEQ ID NO 598
LENGTH: 20
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT LOCATION: (6)...(
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Gaps

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Length 21; 02; 0; Indels

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